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(54) Title: THE ISOLATION AND PRODUCTION OF CATALYTIC ANTIBODIES USING PHAGE TECHNOLOGY

(57) Abstract

Disclosed and claimed are methods for producing catalytic antibodies, including human catalytic antibodies, from bacteriophage. The methods require the cloning, selection, screening, and isolation of catalytic antibodies. Also disclosed and claimed are the products themselves, the catalytic antibodies, made from the phage technology. In addition, catalytic antibodies produced from the phage technology and useful in prodrug activation are disclosed and claimed. And finally, the invention also understands the production of catalytic antibodies to phosphonates.

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THE ISOLATION AND PRODUCTION OF CATALYTIC ANTIBODIES USING PHAGE TECHNOLOGY

REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of International Application WO 92/01047 (PCT/GB91/01134) having an International filing date of July 10, 1991, a publication date of January 23, 1992, and wherein the U. S. is a designated State, said International Application WO 92/01047 (PCT/GB91/01134) being hereby incorporated by reference.

FIELD OF THE INVENTION

The present invention relates to the isolation and production of catalytic antibodies displayed on bacteriophage and, more particularly, the isolation and production of human catalytic antibodies. This invention also relates to the isolation and production of catalytic antibodies for use in prodrug activation. This invention further relates to production of catalytic antibodies that bind to transitional state analogs.

BACKGROUND OF THE INVENTION

Monoclonal antibodies are traditionally made by establishing an immortal mammalian cell line which is derived from a single immunoglobulin producing cell secreting one form of a biologically functional antibody molecule with a particular specificity. Because the antibody-secreting mammalian cell line is immortal, the characteristics of the antibody are reproducible from batch to batch. The key proprieties of monoclonal antibodies are their specificity for a particular antigen and the reproducibility with which they can be manufactured.

Structurally, the simplest antibody (IgG) comprises four polypeptide chains, two heavy (H) chains and two light (L) chains connected by disulfide bonds. The light chains exist in two distinct forms called K (kappa) and λ (lambda). Each chain has a constant region (C) and a variable region (V). Each chain is organized into a series of domains. The light chains have two domains, corresponding to the C region and the other to the V Region. The heavy chains

have four domains, one corresponding to the V region and three domains (1, 2, and 3) in the C region. The antibody has two arms (each arm being a Fab region), each of which has a VL and a VH region associated with each other. It is this pair of V regions (VL and VH) that differ from one antibody to another (owing to amino acid sequence variations), and which together are responsible for recognizing the antigen and providing an antigen binding site (ABS). In even more detail, each V region is made up from three complementarily determining regions (CDR) separated by four framework regions (FR). The CDRs are the most variable part of the variable regions, and they perform the critical antigen binding function. The CDR regions are derived from many potential germ line sequences via a complex process involving recombination, mutation, and selection.

It has been shown that the function of binding antigens can be performed by fragments of a whole antibody. Example binding fragments are (i) the Fab fragment consisting of the VL, VH, CL and CH1 domains; (ii) the Fd fragment consisting of the VH and CH1 domains; (iii) the Fv fragment consisting of the VL and VH domains of a single arm of an antibody; (iv) the dAb fragment (Ward et al., Nature 341 (1989): 544-546) which consists of a VH domain; (v) isolated CDR regions; and (vi) $F(ab')_2$ fragments, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region.

Although the two domains of the Fv fragment are coded for by separate genes, it has proved possible to make a synthetic linker that enables them to be made as a single protein chain (known as single chain Fv (scFv); Bird et al., Science 242 (1988):423-426; Huston et al., Proc. Natl. Acad. Sci., USA 85 (1988):5879-5883); by recombinant methods. These scFv fragments were assembled from genes from monoclonals that had been previously isolated. In our earlier application, WO 92/01047, we described a process to assemble scFv fragments from VH and VL domains that were not part of a previously isolated antibody.

Although monoclonal antibodies, their fragments and derivatives have been enormously advantageous, there are nevertheless a number of limitations associated with them. First, the therapeutic applications of monoclonal antibodies produced by human immortal cell lines holds great promise for the treatment of a wide range of diseases (Lennox, Clinical Applications of

Monoclonal Antibodies, British Medical Bulletin 1984). Unfortunately, immortal antibody-producing human cell lines are very difficult to establish and they give low yields of antibody (approximately 1 μg/ml). In contrast, equivalent rodent cell lines yield high amounts of antibody (approximately 100 μg/ml). However, the repeated administration of these foreign rodent proteins to humans can lead to harmful hypersensitivity reactions. As a result, these rodent-derived monoclonal antibodies have limited therapeutic use.

Second, a key aspect in the isolation of monoclonal antibodies is how many different clones of antibody producing cells with different specificities, can be practically established and sampled compared to how many theoretically need to be sampled in order to isolate a cell producing antibody with the desired specificity characteristics (Milstein, Royal Soc. Croonian Lecture, Proc. R. Soc. London B. 239 (1990):1-16). For example, the number of different specificities expressed at any one time by lymphocytes of the murine immune system is thought to be approximately 10^7 and this is only a small proportion of the potential repertoire of specificities. However, during the isolation of a typical antibody producing cell with a desired specificity, the investigator is only able to sample 10^3 to 10^4 individual specificities. The problem is worse in the human, where one has approximately 10^{12} lymphocyte specificities with the limitation on sampling of 10^3 or 10^4 remaining.

This problem has been alleviated to some extent in laboratory animals by the use of immunization regimes. Thus, where one wants to produce monoclonal antibodies having a specificity against a particular epitope, an animal is immunized with an immunogen expressing that epitope. The animal will then mount an immune response against the immunogen and there will be a proliferation of lymphocytes which have specificity against the epitope. Owing to this proliferation of lymphocytes with the desired specificity, it becomes easier to detect them in the sampling procedure. However, this approach is not successful in all cases as a suitable immunogen may not be available. Furthermore, where one wants to produce human monoclonal antibodies (e.g., for therapeutic administration), such an approach is not practically or ethically feasible.

In our earlier application, WO 92/01047, we described methods of constructing a bacteriophage that expresses and displays at its surface a large biologically functional binding molecule (e.g., antibody fragments, enzymes, and receptors) and which remains intact and infectious. We called the structure which comprises a virus particle and a binding molecule displayed at the viral surface a "package". Where the binding molecule is an antibody, an antibody derivative or fragment, or a domain that is homologous to an immunoglobulin domain, we called the package a "phage antibody" (pAb). However, except where the context demanded otherwise, where the term phage antibody is used generally, it was also interpreted as referring to any package comprising a virus particle and a biologically functional binding molecule displayed at the viral surface. Since the original filing of WO 92/01047, a number of examples of functional antibody and other protein domains expressed on the surface of bacteriophage have been reported in both the literature and additional patent applications.

This simple substitution of immortalized cells with bacterial cells as the "factory", considerably simplifies procedures for preparing large amounts of binding molecules expressed on the surface of the bacteriophage. Furthermore, the use of polymerase chain reaction (PCR) amplification (Saiki et al., Science 239 (1988):487-491) to isolate antibody producing sequences from cells (e.g., hybridomas and B cells) has great potential for speeding up the timescale under which binding specificities can be isolated. Phage antibody expression libraries can be easily generated by cloning the amplified VH and VL genes directly into bacteriophage expression vectors. Furthermore, a bacteriophage based recombinant production system allows scope for producing tailor-made antibodies and fragments thereof. For example, it is possible to produce chimeric molecules with new combinations of binding and effector functions, humanized antibodies (e.g., murine variable regions combined with human constant domains or murine-antibody CDRs grafted onto a human FR) and novel antigen-binding molecules. The key advantage of the phage based system being the ability to directly screen the recombinant antibodies directly for the desired binding specificities.

In creating recombinant VH and VL phage libraries several problems need to be addressed. For example, in a mouse there are approximately 10^7 possible H chains and 10^7

possible L chains. Therefore, there are 10^{14} possible combinations of H and L chains, and to test for anything like this number of combinations, one would have to create and screen a library of about 10^{14} clones. This had not previously been a practical possibility. PCT/GB92/00883 and PCT/GB92/01755 applications, which are herein incorporated by reference, disclose a number of approaches which ameliorate this problem. Each of these applications is a continuation-in-part of our International Application WO 92/01047.

In addition, a number of molecular biological techniques which have previously been developed for engineering of antibody active sites can be applied in combination with the phage antibody library approaches described previously. These techniques include site-directed mutagenesis of residues within a CDR, replacement of all or portions of CDR (s) with random amino acid sequence, CDR shuffling in which a CDR region is essentially replaced with a library of CDR regions. The use of pAbs may also allow the construction of entirely synthetic antibodies. Furthermore, antibodies may be made which have some synthetic sequences, for example, CDRs, and some naturally derived sequences (see for example PCT/BG92/06372). For example, V-gene repertoires could be made *in vitro* by combining un-rearranged V genes, with D and J segments. Libraries of pAbs could then be selected by binding to antigen, hypermutated *in vitro* in the antigen-binding loops or V domain framework regions, and subjected to further rounds of selection and mutagenesis.

pAbs have a range of applications in selecting antibody genes encoding antigen binding activities. One particularly exciting area of application is in the development of antibodies with catalytic properties (catalytic antibodies). Catalytic antibodies have been described in U.S. Patent Nos. 4,888,281 to Schochetman et al.; 4,963,355 to Kim et al.; and 5,037,750 to Schochetman et al., all hereby incorporated by reference. As disclosed therein, catalytic antibodies combine the catalytic abilities of enzymes with the binding capabilities of antibodies.

All catalytic antibodies described to date have been generated using monoclonal antibody technology. The details of that process are well known to those of ordinary skill in the art. A typical methodology first involves immunizing mice with an appropriate antigen. The antigen may be the desired reactant; the desired reactant bound to a peptide or other carrier

molecule; a reaction intermediate or an analog of the reactant; or the product or a reaction intermediate.

"Analog" as the term is used here can encompass isomers, homologs, transition state analogs or other compounds sufficiently resembling the reactant in terms of chemical structure such that an antibody raised against the analog may participate in an immunological reaction with the reactant but will not necessarily catalyze a reaction of the analog.

Although a number of different types of antibody catalysts have been developed with this technology, the time required to establish and then screen the hybridomas for the desired specificity is of considerable importance.

If the desired specificity is sufficiently rare, it may be impractical or impossible to sample enough hybridomas cell lines to recover the desired specificity.

Additionally, there is currently no suitable hybridoma based technology for generating entirely human catalytic antibodies.

The methods of the invention can also be used to effect a cleavage that leads to the activation of some biological function.

Such reactions include the cleavage of peptide bonds, but may also include ester bonds or glycosidic bonds or other types of bonds.

One example of the cleavage of a biomolecule which leads to the activation of a biological function is the treatment of insulin-dependent diabetes. Patients self-administer insulin by injection. Prior attempts to develop a formulation of insulin whose release into the circulation mimics the pharmacokinetics of the release of natural pancreatic insulin have not proved successful. Insulin exists in the pancreas in a pro-form, proinsulin, whose activity is many orders of magnitude lower than insulin itself. An antibody protease specific for the peptide bond that leads to conversion of proinsulin to insulin can be designed so that its kinetic characteristics allow release of insulin *in vivo* after an injection of proinsulin plus antibody protease. This is an example of prodrug activation where the drug in this instance is a natural protein hormone. Prodrugs may include many therapeutically active molecules which lead to the activation or deactivation of a biological function. The pro-form may either take advantage

of a natural modification of the drug or any suitable synthetic modification thereof. Suitable drug derivatives with low activity (therapeutically beneficial or toxic), which, on modification with a suitable catalytic antibody, are converted to an active form. A particular example of this process is given in PCT/US89/01951 filed May 4, 1989, which is hereby incorporated by reference.

SUMMARY OF THE INVENTION

One object of the present invention is to provide a method for producing and isolating a catalytic antibody displayed on phage which is capable of catalytically increasing the rate of a chemical reaction.

Another object of the present invention is to produce human catalytic antibodies by one of several different methods outlined hereafter.

A further object of the present invention is to isolate phage displaying antibody epitopes that bind to transition state analogs, phosphonates, and RT3.

Still another object of the present invention is to produce a catalytic antibody from antibodies (either mouse or human-derived) that bind transition state analogs, phosphonates, and RT3 by one of several different methods including mutagenesis, chain shuffling, and CDR shuffling or various combinations of these procedures.

And finally, yet another object of the present invention is to produce catalytic antibodies for use in prodrug activation.

Accordingly, the present invention provides a method for producing catalytic antibodies displayed on phage comprising the steps of:

(a) generating a gene library of antibody-derived domains;

(b) inserting coding for said domains into a phage expression vector; and

(c) isolating said catalytic antibodies.

The invention further provides a method for isolating catalytic antibodies displayed on phage comprising the following steps:

(a) preparing an antigen;

(b) immunizing with said antigen;

(c) generating a library of VH and VL domains from said immunized animal;

(d) cloning said VH and VL domains into a phage expression vector to generate phage display antibodies;

(e) selecting phage display antibodies which bind specifically to said antigen;

(f) screening said selected phage display antibodies for catalytic activity to substrate; and

(g) isolating said catalytic antibodies.

The invention further provides a method for isolating catalytic human antibodies displayed on phage comprising the following steps:

(a) preparing an antigen;

(b) generating a library of VH and VL domains;

(c) cloning said VH and VL domains into a phage expression vector to generate phage display antibodies;

(d) selecting phage display antibodies which bind specifically to said antigen;

(e) screening said selected phage display antibodies for catalytic activity to substrate; and

(f) isolating said catalytic antibodies.

The invention further provides a method for producing catalytic antibodies displayed on phage through chain shuffling comprising the following steps:

(a) combining a library of VL genes with VH genes to form a chain shuffled library;

(b) cloning the shuffled chain;

(c) expressing said catalytic antibody on phage;

(d) selecting against an antigen; and

(e) screening for catalytic activity.

The invention further provides a method for producing catalytic antibodies displayed on phage through CDR shuffling comprising the following steps:

(a) isolating VL and VH genes;

(b) isolating a library of CDR regions;

(c) recombining said VL and VH genes with said library of CDR regions to produce a CDR shuffled library; and

(d) cloning the CDR shuffled library;

(e) expressing said CDR shuffled library on phage;

(f) selecting against an antigen; and

(g) screening for catalytic activity.

The invention further provides a method for producing catalytic antibodies displayed on phage through imprinting comprising the following steps:

(a) selecting a set of antibodies;

(b) isolating a set of VH and a set of VL genes from said antibodies;

(c) combining said set of VH with a library of VL and combining said set of VL with a library of VH to form two combination libraries;

(d) cloning said combination libraries;

(e) expressing said libraries on phage;

(f) selecting against an antigen;

(g) isolating selected libraries of VH and VL genes;

(h) combining said libraries of VH and VL genes;

(i) cloning said combined libraries;

(j) expressing said combined libraries on phage;

(k) reselecting against an antigen; and

(l) screening for catalytic activity.

The invention further provides a method for enhancing the rate of cleavage or formation of a specific bond within a molecule *in vivo* which comprises introducing into an animal an effective amount of a phage-derived catalytic antibody.

The invention further provides a method for *in vivo* activation of a prodrug comprising:

(a) introducing a prodrug into a patient, said prodrug having a chemical bond therein which upon cleavage releases the active form of said drug; and

(b) introducing into said patient an effective amount of a phage-derived catalytic antibody capable of cleaving said bond in said prodrug.

BRIEF DESCRIPTION OF THE DRAWINGS

The present invention as defined in the claims can be better understood with reference to the text and to the drawings.

FIGS. 1-4 show the reaction schemes for the synthesis of Compounds 7 (RT3 hapten), 8, 12, and 15, respectively, and intermediates thereof.

FIG. 5 shows the plasmid construct resulting from the insertion of His-6 oligo into pHEN-OX16 to give pHEN-OX16his11.

FIG. 6 shows an SDS polyacrylanide gel starved with coomassie are:

(a) total periplasmic proteins from 1 ml of cells.

(b) unbound fraction from 1 ml of cells, after addition of binding matrix.

(c) fraction bound and eluted from matrix, equivalent to 1 ml of cells.

(d-f) are purified fractions equivalent to 5 mls of cells.

(d) pOX16-his-11 antibody fragment eluted with PBS+1M Nacl, 250 mM imidazole.

(e) pOX16-his-11 antibody fragment eluted with PBS, 250 mM imidazole.

(f) pSCFv4his-6 antibody fragment eluted with PBS+1M NaCl, 250 mM imidazole.

FIG. 7 shows pCANTAB vectors encoding C terminal his-6 peptides.

FIG. 8 shows the competitive assay results for selected mouse RT3 phage antibodies with haptens (RT3) portions of the haptens (RT3A and RT3B) or portions of the product (Prod A and Prod B).

FIG. 9 shows the genetic sequence of light chain pattern A and light chain pattern C from mouse-derived RT3 phage antibodies.

FIG. 10 shows the alignment of the mouse germline to the genetic sequence of light chain pattersn B, D, and I from mouse-derived RT3 phage antibodies.

FIG. 11 shows the comparison of genetic sequences of light chain patterns A, B, C, D, and I from mouse-derived RT3 phage antibodies.

FIG. 12 shows the genetic sequence of heavy chain pattern A from mouse-derived RT3 phage antibodies.

FIG. 13 shows the alignment of the mouse germline to the genetic sequence of heavy chain patterns B and D from mouse-derived RT3 phage antibodies.

FIG. 14 shows the comparison of genetic sequences of heavy chain patterns A, B, C, D, and I from mouse-derived RT3 phage antibodies.

FIG. 15A shows an HPLC chromatogram of a catalytic assay of IMAC

pure scFv from clone 18.

FIG. 15B shows an HPLC chromatogram of a catalytic assay + RT3 hapten of IMAC pure scFv from clone 18

FIG.15C shows an HPLC chromatogram of a catalytic RT3 assay blank at pH 9.0

FIG. 16 shows an HPLC chromatogram of a catalytic assay of HIC pure scFv from clone 18.

FIG. 17A shows an HPLC chromatogram of a catalytic assay of IMAC pure scFv from clone 83.

FIG. 17B shows an HPLC chromatogram of a catalytic assay + RT3 hapten of IMAC pure scFv from clone 83

FIG. 18 shows an HPLC chromatogram of a catalytic assay of HIC pure scFv from clone 83

FIG. 19A shows binding pattern of clones to RT3 obtained after 3 rounds of panning of a naive human-derived phage antibody library.

FIG. 19B shows binding pattern of clones to RT3 after 4 rounds of panning of a naive human-derived phage antibody library.

FIG. 20 shows genetic sequences of heavy and light chains of RT3 specific phage antibodies selected from a naive human phage antibody library.

FIG. 21 shows the general scheme for VH and VL chain shuffling.

FIG. 22 shows RT3-BSA ELISA assay with polyclonal phage derived from human shufflid libraries after PAN0, PAN1, and PAN2.

FIG. 23A shows inhibitoin of phage antibody bidning to RT3-BSA by left hand portion of RT3 hapten (RT3A) or substrate (Product A).

FIG. 23B shows inhibition of phage antibody binding to RT3-BSA by right hand portion of RT3 hapten (RT3B) or substrate (Product B).

FIG. 24A shows yield of phage eluted with RT3, RT3A, RT3B, TEA and PBS from ELISA wells coated with 0.3 μg of RT3-BSA.

FIG. 24B shows yield of phage eluted with RT3, RT3A, RT3B, and TEA from ELISA wells coated with 15 μg of RT3-BSA.

In order that the invention herein described may be more fully understood, the following detailed description is set forth. This description, while exemplary of the present invention, is not to be construed as specifically limiting the invention and such variations which would be within the purview of one skilled in this art are to be considered to fall within the scope of this invention.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

For the sake of convenience and ready reference, the following definitions will be used in describing the instant invention.

Analog encompasses isomers, homologs, transition states or other compounds

sufficiently resembling the reactant in terms of chemical structure such that an antibody raised against an analog may participate in an immunological reaction with the reactant but will not necessarily catalyze a reaction of the analog.

Antibody describes an immunoglobulin whether natural or partly or wholly synthetically produced. The term also covers any protein having a binding domain which is homologous to an immunoglobulin binding domain. These proteins can be derived from natural sources, or partly or wholly synthetically produced. Example antibodies are the immunoglobulin isotopes and the Fab, $F(ab1)_2$, scFv, fV, dAb, Fd fragments.

An antibody-derived domain refers to a sequence derived from an antibody molecule.

Antigen is a substance, frequently a protein, that can stimulate an animal organism to produce antibodies and that can combine with the antibodies these produced.

A domain is a part of a protein that is folded within itself and independently of other parts of the same protein and independently of a complementary binding member.

Homologs indicate polypeptides having the same or conserved residues at a corresponding position in their primary, secondary, or tertiary structure. The term also extends to two or more nucleotide sequences encoding the homologous polypeptides. Examples of homologous peptides are the immunoglobulin isotopes.

Isolating refers to the separation of a specific phage from the library.

Library is a collection of oligo or polynucleotides, e.g., DNA sequences within clones.

A naive library is a phage display library of immunoglobulin sequences derived from an animal which has not been immunized with the following: the reactant; the reactant bound to a peptide or other carrier, a reaction intermediate; an analog of the reactant; an analog of the product in which the antibody so generated is capable of binding to the reactant or a reaction intermediate; and an analog of a reaction intermediate or transition state.

A package describes a replicable genetic display package in which the particle is displaying a member of a sbp at its surface. The package may be a bacteriophage which displays an antigen binding domain at its surface. This type of package has been called a phage antibody (pAb).

A phage vector is a vector derived by modification of a phage genome, containing an origin of replication for a bacteriophage, but not one for a plasmid.

A phagemid vector is a vector derived by modification of a plasmid genome, containing an origin of replication for a bacteriophage as well as the plasmid origin of replication.

A vector is a DNA molecule, capable of replication in a host organism, into which a gene is inserted to construct a recombinant DNA molecule.

An Overview Of The Method

The invention describes methods to generate and isolate phage particles which express on their surface an antibody with catalytic properties. In the practice of the invention the antibody domains encoding the catalytic functionality can be prepared from either specifically immunized or non-immunized animal or human sources as defined below. Additionally, the invention describes methods of generating or improving binding and/or catalytic function by one of several methodologies including but not limited to chain shuffling, CDR grafting, and mutagenesis. In a further embodiment of the invention, a method is disclosed for converting a catalytic antibody encoded entirely by mouse-derived VH and VL domains into one encode by human-derived VH and VL domains

The first step in generating antibodies with specific catalytic function requires, but is not necessarily limited to, a chemical hapten (e.g., transition state analog (TSA) that is related to, but distinct from the substrate of the reaction to be catalyzed). The structure, synthesis, and use of said TSA(s) as a means to generate antibodies with catalytic function has been described in U.S. Patent No. 4,196,265 issued April 1, 1980, which is hereby incorporated by reference. As described in the prior art, the traditional route for producing and isolating catalytic antibodies has been through a monoclonal antibody approach (hybridoma technology).

The present invention utilizes a phosphonate transition state analog as either an immunogen or immobilized on a solid phase to allow generation and selection of antibodies which bind said TSA and which may have catalytic properties (see FIG.1). Unlike previous inventions in which catalytic antibodies are produced via hybridoma methods, the unique

embodiment of the invention is the ability to express antibody domains, including those with catalytic function, on the surface of a bacteriophage. Methods for generating libraries of phage with the potential for displaying catalytic antibody domains on their surface are described in detail below.

1. Production Of Binding and/or Catalytic Phage Antibodies From An Immunized Source

The TSA is bound to a carrier molecule or peptide and immunized into BALB/C mice. After an appropriate amount of time spleens are removed from the mice and mRNA isolated from the cells. The RNA serves as a starting source material for amplifying immunoglobulin variable domains for cloning into bacteriophage expression vector and subsequent expression on the surface of bacteriophage particle. In the embodiment of this invention the variable domains are typically linked by a short peptide to produce a scFv as described in the background to the present invention. It should be noted that alternative phage expression vectors could be used for expression of the antibody as Fab. Techniques for creating said phage antibody libraries have been described previously and the details of the process are well known to those skilled in the art. (see, e.g., WO 92/01047; McCafferty et al., Nature (1990):552-564.; Hoogenboom et al., Nucl. Acids. Res. (1991):4133-4137; Marks et al., J. Mol. Biol. (1991):581-597).

Phage antibodies which specifically bind and recognize the TSA are isolated from the library by one of several methods as described below:

a) Panning - TSA is immobilized directly on a solid surface (i.e., tube or plate) or alternatively coupled to a carrier protein prior to coating the solid phase surface. A suspension containing the library of phage antibodies is allowed to react with the coated surface for some time after which unbound phage antibodies (those that do not bind the TSA) are removed by washing.

b) Affinity Chromatography - TSA is coupled to a suitable column matrix (i.e., Sepharose). Phage antibody suspension is passed over the column and unbound phage are washed through the column with buffer.

Phage antibodies that bind and are immobilized on the solid phase surface can be removed by one of several methods including:

a) Non-specific elution by using buffers of either low (acidic) or high (basic) pH.

b) Specific elution with free hapten such as the original phosphonate TSA or substrate or product of the reaction

c) Specific elution with portions of the TSA, or substrate or product.

In addition to specific elution of phage antibodies bound to the TSA, it may be desirable to control the binding of the phage antibodies during the initial panning or affinity chromatography step. One method would be to use competitive inhibition in which the phage antibodies are first preincubated with reactants, reaction products or portions of the TSA (see Example 9). The purpose of such "preselection" would be to eliminate from the population of binding antibodies those least likely to be catalytic. In the context of the present example, those eliminated would be phage antibodies that do not substantially bind the phosphonate portion of the TSA. The type of preselection of the phage antibody library would need to be determined experimentally, but ultimately could lead to methods to enrich within the population of TSA binding phage antibodies the proportion of catalytic over non-catalytic phage. A greater degree of flexibility could be exerted if such procedures were carried out in ELISA wells. Thus, following a particular procedure, the eluate could be collected and the whole plate carried through a detection procedure. Based on the results, the eluate from specific wells could be selected for further analysis/pannings.

Following elution of phage antibodies by any or all of the above methods, phage are collected and can be subjected to additional pannings (2, 3, 4, 5, etc.) simply by collecting the eluted phage from the previous panning and reincubating on TSA solid phase. Since, a certain percentage of phage that do not specifically bind to the TSA are carried through each panning step (i.e., non-specific binders), pools of phage clones or individually isolated phage clones are typically rescreened for binding to the TSA by a solid phase ELISA assay. The ELISA assay can be done with antibody expressed on the bacteriophage surface or expressed in a

soluble form as described below. Other formats of the ELISA assay, for example competitive inhibition with free hapten, substrate or product or various halves or portions of said hapten, substrate or product can be employed to further characterize the binding specificity of the pools of phage clones or individual binding clones.

Individual phage antibody clones or pools of clones which have the appropriate binding specificity are then assayed for catalytic activity. Assay for catalysis is most conveniently done using soluble antibody and methods for producing soluble antibody from a phage antibody expressing *E. coli* clone have been described previously (Marks et al, J. Mol. Biol. (1991):581-597). A criteria for attributing catalytic activity to the antibody active site is rigorous purification of the antibody away from contaminating proteins or enzymes. In this invention, purification of the soluble antibody is facilitated by incorporation of specific peptides at the 3' carboxyl terminus of the expressed antibody. Examples of such peptides currently used and as reported in the prior art include:

a) histidine peptide - allows purification of antibody on metal immobilized on a column matrix (IMAC, Hochuli et al., Bio/Technology (1988):1321-1325).

b) myc peptide - allows purification on a column matrix on which antibody that binds specifically to the myc peptide has been immobilized (Clackson et al. Nature (1991):624-628).

Previous vectors utilized for display of antibody fragments contained only the myc peptide (see FIG. 5). The vectors described and disclosed in this application represent the first example of incorporation of the histidine peptide in tandem with the myc peptide. This represents an improvement over the previous art because it allows purification of the soluble antibody using two uniquely different formats and purification conditions.

Additional purification of antibody can be achieved by utilizing specific properties unique to the antibody of interest such as hydrophobicity, charge, and size. Purification is affected by any of a number of standard protein purification techniques as described previously (Deutscher, Methods in Enzymology, Vol. 182, Guide to Protein Purification (1990).

Antibodies isolated by phage antibody techniques described above can be screened for the ability to catalyze the desired reaction by a number of methods well known in the art. In its simplest form screening is accomplished by incubating antibody and reactant (substrate) under appropriate conditions and measuring the formation of product by any of a number of means such as spectrophotometric methods or high pressure liquid chromatography.

2. Production Of Binding and/or Catalytic Phage Antibodies From A Non-immunized Source

In this embodiment of the invention source material for generating a phage antibody library is from a non-immunized animal or mammal such as human. Non-immunized in this example means not specifically immunized with a specific reactant (either bound to a carrier protein or as free reactant), reaction intermediate, analog of a reactant or expected products of a particular reaction. As demonstrated in the prior art, low and moderate affinity human antibodies have been generated to specific antigens using phage antibody libraries generated from a non-immunized source. Such an approach provides a method for generating animal or human antibodies that bind to a TSA simply by panning the naive animal or human derived phage antibody library on TSA as described above. Phage clones which specifically bind and recognize the TSA can then be assayed for the desired catalytic function as described. Such an approach provides a method to isolate directly an entirely human derived catalytic antibody.

3. Production Of Binding and/or Catalytic Phage Antibodies By Chain-Shuffling

A chain-shuffling approach for generating phage antibody libraries takes advantage of the promiscuity of binding between VH and VK pairs. In this embodiment of the invention, the VH or VK domain from one, several or many different phage antibody clones is recombined with a library of VK or VH domains. The phage clones and libraries of VH and VK domains can be obtained from an immunized source as described in Section 1 above or an non-immunized source as described in Section 2 above. In addition, the phage clones chosen for chain shuffling can be, but is not necessarily limited to, those that have previously been

selected for binding to a particular TSA. Following the chain shuffling procedure the recombined chains (i.e., shuffled chains) are cloned back into the phage antibody expression vector. The expressed phage antibody library is repanned on the TSA and individual binding clones screened for catalytic activity as earlier described.

4. Production of Binding and/or Catalytic Phage Antibodies by CDR Shuffling

It is well known that antibody specificity and antigen binding affinity are specified by the six CDR's encoded by the VH and VL domains. It follows then that altering any or all of the CDR's from a given antibody will have dramatic effects on the binding properties of that antibody. CDR shuffling as it relates to phage antibodies describes a process for replacing a region encoding a CDR or CDR's within a VH or VL domain with a library of CDR or CDR's. As with the chain shuffling approach described in Section 3 above, the VH or VK domain used for CDR shuffling can be from one, several or many different phage antibody clones. The phage clones and libraries of CDR regions used for shuffling can be obtained from either immunized or non-immunized sources. Following CDR shuffling the recombinant VH and VL domains are recloned into the phage antibody expression vector. The expressed phage antibodies are repannned against the TSA and individual binding clones assayed for catalytic activity as described above.

5. Production of Binding and/or Catalytic Phage Antibodies by Mutagenesis

As described above for CDR shuffling binding specificity of an antibody can be altered by changing amino acids encoded within CDRs. CDR mutagenesis for the purposes of this invention can be defined as:

a) site-directed in which one or a few specific amino acids within a particular CDR are mutagenized. This process normally results in alteration of the wild-type amino sequence to several different amino acids dependent upon the nucleotide sequence of the region being mutagenized and the sequence of the mutagenic primer.

b) random mutagenesis in which some or all of the amino acids within a CDR or CDRs is replaced with a random nucleotide sequence such that the wild type sequence is replaced by all possible combinations of amino acids.

A number of different methodologies for both site-directed and random mutagenesis have been described in the literature and are well known to those in the art. As with the other methodologies, the phage antibody clone or clones chosen for mutagenesis could be, but is not limited to, ones already selected for binding to the TSA. In addition, the chosen binding clones could be ones isolated from phage antibody libraries derived from either immunized or non-immunized animal or human sources.

Recent successes in modelling antigen binding sites augurs well for *de novo* design. The approach is especially attractive for making, catalytic antibodies, particularly for small substrates. Here side chains or binding sites for prosthetic groups might be introduced, not only to bind selectively to the transition state of the substrate, but also to participate directly in bond making and breaking.

6. Derivation of Human Catalytic Antibodies by "imprinting"

The process of "imprinting" involves using an existing antibody with desired binding characteristics, to derive new antibodies, with similar characteristics. This is done by recombining original antibody chains, or parts thereof, with a library of complementary parts. When new antibody elements are found, which complement the original antibody binding characteristics, these are recombined with a library which replaces the original antibody binding characteristics, these are recombined with a library which replaces the original antibody part, to give an entirely new antibody which mimics the binding of the original antibody (PCT/GB/92/01755).

For example, an imprinting approach would have value for humanizing a mouse catalytic antibody isolated using phage antibody technology as described in Section 1 above. Once isolated, the mouse encoded VH or VL domain of the catalytic antibody could be recombined with a library of the complimentary human derived VL or VH domains. The half

mouse-half human phage antibodies are then reselected for binding to the TSA used originally to generate the catalytic activity. The remaining mouse VH or VL domain of the selected binders is now replaced with a library of the complimentary human derived VL or VH domains. The resulting phage antibodies which now are encoded entirely by human derived sequences entirely are again reselected for binding to the TSA. Individual clones selected for binding to the TSA are then assayed as described above for catalytic activity.

Having now generally described this invention, the following examples are included for purposes of illustration and are not intended as any form of limitation.

Example 1.1

Synthesis of RT3 Phosphonate Transition State Analog Hapten

The reaction scheme for the synthesis of the RT3 phosphonate transition state analog is shown in Figure 1. α2-Chloroisodurene (1) by halogen exchange using sodium iodide in acetone gave α2-Iodoisodurene (2). Michaelis-Arbusov reaction with trimethylphosphite yielded the dimethoxy phosphonate compound (3). Activation by heating with phosphorus pentachloride and subsequent reaction with Methy 4-Hydroxyphenylacetate (4) afforded compound (5). Demethylation using thiophenol and triethylamine produced compound (6) which under strong basic conditions of lithium hydroxide was fully deprotected to the derised product (7).

More specifically, α2-Iodoisodurene (Compound 2) was prepared as follows:

α2-Chloroisodurene (Compound 1) (2.28 g) was dissolved in acetone (45 ml) and NaI (2.25 g) was added. The reaction mixture was stirred vigorously at 75° C in the dark for 16 hours. The reaction mixture was concentrated, redissolved in ethyl acetate (100 ml), washed with water and concentrated to a solid. The solid was redissolved in ethyl acetate (5 ml) and purified by flash chromatography using 100 g of silica and eluting with hexane to give α2-

Iodiosodurene (2) (2.717 g). This was confirmed by spectroscopy ^{1}H NMR ($CDCl_3$) δ 2.25 (s,3H), 2.33 (s, 6H), 4.48 (s, 2H), 6.85 (s, 2H).

Preparation of Compound 3

Freshly distilled Trimethoxyphosphite (5 ml) and α2-Iodoisodurene (2) (0.765 g) were heated together at 110° C for 16 hours. Te reaction mixture was concentrated to a small volume and purified by flash chromatography using 50 g of silica and eluting with ethyl acetate-hexane (2:8 volume by volume) to give compound 3 (0.550 g). This was confirmed by spectroscopy - ^{1}H NMR ($CDCl_3$) δ 2.25 and 2.27 (2s, 3H), 2.40 (1s, 6H), 3.25 (d, 2H), 3.65 (d, 6H), 6.88 (s, 2H).

Methyl 4-Hydroxyphenylacetate (Compound 4)

4-Hydroxyphenylacetic acid (1.75 g) was dissolved in methanol (30 ml) and 10 M aqueous hydrochloric acid (0.15 ml) was added and heated to reflux for 15 hours. After cooling to room temperature, triethylamine (1 ml) was added, the mixture concentrated, purified by flash chromatography using silica gel (30 g) and eluted with ethyl acetate-hexane (2:8 volume by volume) to give Methyl 4-Hydroxyphenylacetate (4) (1.693 g). This was confirmed by spectroscopy - ^{1}H NMR ($CDCl_3$) δ 3.58 (s, 2H), 3.73 (s, 3H), 6.75 (d, 2H), 7.10 (d, 2H).

Preparation of Compound 5

Compound 3 (0.243 g) was dissolved in dry chloroform (3 ml) and a solution of phosphorus pentachloride (0.240 g) in dry chloroform (3 ml) added followed by heating at 60° C for 3 hours. The reaction mixture was concentrated to an oil which was left to stir under high vacuum for 16 hours. The resultant phosphorochloridate was redissloved in dry dichloromethane (3 ml) and added to a solution of Methyl 4-Hydroxyphenylacetate (4) (0.150

g) and 4-Dimethylaminopyridine (0.146 g) in dry dichloromethane (3 ml) at 0° C. The reaction mixture was stirred at room temperature for 16 hours. Saturated aqueous ammonium chloride (15 ml) was added and products were extracted into dichloromethane (40 ml). The organic layer was washed with water (10 ml), dried over anhydrous $MgSO_4$, filtered and concentrated then purified by flash chromatography using silica (30 g) and eluting with ethyl acetate-hexane (4:6 volume by volume) to give compound 5 (0.20 g). This was confirmed by spectroscopy - ^1H NMR ($CDCl_3$) δ 2.27 and 2.30 (2s, 3H), 2.40 and 2.42 (2s, 6H), 3.40 (d, 2H), 3.58 (s, 2H), 3.67 (d, 3H), 3.69 (s, 3H), 6.88 (s, 2H), 7.05 (d, 2H), 7.20 (d, 2H).

Preparation of Compound 6

Compound 5 (0.19 g) was dissolved in dioxane (1.5 ml). Thiophenol (0.575 g) and triethylamine (0.70 ml) were added and the reaction mixture was stirred for 16 hours. The mixture was concentrated, redissolved in water (30 ml) and washed with dichloromethane (5 x 25 ml). The aqueous layer was adjusted to pH 1 with aqueous HCl and extracted with ethyl acetate (5 x 30 ml). The organic layers were combined, dried over anhydrous $MgSO_4$, filtered and concentrated to give compound 6 (0.176 g). This was confirmed by spectroscopy - ^1H NMR ($CDCl_3$) δ 2.15 (bs, 3H), 2.28 (bs, 6H), 3.13 (d, 2H) 3.40 (bs, 2H), 3.60 (bs, 3H), 6.68 (bs, 2H), 6.85 (bs, 2H), 7.00 (bs, 2H).

Preparation of Compound 7

Compound 6 (0.087 g) was treated with a solution of lithium hydroxide monohydrate (0.025 g) in methanol (1.4 ml) and water (0.30 ml) with vigorous stirring for 50 hours. The reaction mixture was concentrated to a third of its volume, water (10 ml) was added and the aqueous layer was washed with dichloromethane (3 x 10 ml). The aqueous layer was adjusted to pH 1 with concentrated HCl and was extracted with ethyl acetate (7 x 20 mL). Organic layers were combined, dried over anhydrous $MgSO_4$, filtered and concentrated to give

compound 7 (0.063 g). This was confirmed by spectroscopy - ^{1}H NMR (d_6 DMSO) δ 2.170 and 2.175 (2s, 3H), 2.30 (s, 6H), 3.20 (d, 2H), 3.50 (s, 2H), 6.80 (s, 2H), 7.00 (d, 2H), 7.20 (d, 2H).

Example 1.2

Synthesis of Left Hand Portion (Compound 8) of RT3 Phosphonate Transition State Analog (RT3A) (see FIG. 2)

Preparation of Compound 8 from the demethylation of compound 3 using thiophenol and triethylamine.

Compound 3 (0.122 g) was dissolved in dioxane (1.5 ml) and with stirring a solution of thiophenol (0.55 g) in dioxane (1.5 ml) was added. Triethylamine (0.70 ml) is then added and the solution is stirred for 24 hours at room temperature. Reaction mixture was transferred to a separating funnel, water (50 ml) was added, the aqueous layer was adjusted to pH 7 with aqueous HCl and then it was washed with dichloromethane (5 x 50 ml). The aqueous layer was acidified to pH 1 with 1 M aqueous HCl and extracted with ethyl acetate (2 x 75 ml). The organic layers were combined and washed with water (5 ml), dried over anhydrous $MgSO_4$, filtered and concentrated. Purification using silica (10 g) and eluting with methanol-dichloromethane (8:92 volume by volume - 15:85 volume by volume) gave compound 8 (0.055 g). This was confirmed by spectroscopy - ^{1}H NMR (d_6 DMSO) δ 2.10 (bs, 3H), 2.28 (bs, 6H), 3.2 (d, 2H), 3.30 (d, 3H), 6.85 (s, 2H).

Example 1.3

Synthesis of Right Hand Portion (Compound 12) of RT3 Phosphonate Transition State Analog (RT3B) (see FIG. 3)

Preparation of Dibenzylmethylphosphorate (Compound 9)

Sodium hydride (60% dispersion in mineral oil) (0.16 g) was washed with dry hexane (2 x 10 ml). To the decanted solid, dry THF (5 ml) was added and the stirred suspension was cooled to 0° C. A solution of Dibenzyl phosphite (1.048 g) in dry THF (5 ml) was added and the mixture warmed to room temperature. After 30 minutes, methyl iodide (0.32 ml) was added and the reaction mixture stirred for 2 hours. The reaction mixture was concentrated, redissolved in ethyl acetate (75 ml), washed with saturated aqueous ammonium chloride solution (50 ml) and water (10 ml). The organic layer was dried over anhydrous $MgSO_4$, filtered, concentrated then purified by flash chromatography using silica (10 g) and eluting with ethyl acetate-hexane (1:1 volume by volume) which gave Dibenzylmethylphosphonate (9) (0.750 g). This was confirmed by spectroscopy - ^1H NMR ($CDCl_3$) δ 1.48 (d, 3H), 5.00 (m, 4H), 7.40 (s, 10H).

Preparation of Benzylmethylphosphoric Acid (Compound 10)

Dibenzylmethylphosphonate (9) (0.277 g) was dissolved in dioxane (1 ml) and water (0.5 ml). Aqueous 2 M LiOH (1 ml) was added and the mixture was vigorously stirred for 48 hours. Water (25 ml) was added and the aqueous layer was washed with ethyl acetate (25 ml). The aqueous layer was acidified to pH 1 with concentrated HCl and extracted with ethyl acetate (2 x 35 ml). Organic layers were combined, dried over anhydrous $MgSO_4$, filtered and concentrated to give Benzylmethylphosphoric acid (10) (0.183 g). This was confirmed by spectroscopy - ^1H NMR ($CDCl_3$) δ 1.53 (d, 3H), 5.08 (d, 2H), 7.40 (m, 5H), 11.90 (s, 1H).

Preparation of Compound 11

Benzylmethylphosphoric acid (10) (0.118 g) was dissolved in thionyl chloride (1 ml) and stirred for 4 hours. The reaction mixture was concentrated to dryness and was left under high vacuum for 16 hours. This was redissolved in dry dichloromethane (1 ml) and DMF (1.5 ml). With stirring Methyl 4-Hydroxyphenyl acetate (4) (0.083 g) and triethylamine (0.170

mL) was added. After 16 hours, saturated aqueous ammonium chloride (30 ml) was added and the mixture was extracted with ethyl acetate (2 x 50 ml). Organic extracts were combined, dried over anhydrous $MgSO_4$, filtered and concentrated. Purification was achieved using preparative tlc plates (1 mm) and using ethyl acetate-hexane (4:6 volume by volume) as the solvent to give compound (11) (0.068 g). This was confirmed by spectroscopy - ^1H NMR ($CDCl_3$) δ 1.67 (d, 3H), 3.60 (s, 2H), 3.73 (s, 3H), 5.15 (m, 2H), 7.13 (d, 2H), 7.25 (d, 2H), 7.40 (s, 5H).

Preparation of Compound 12

Methylation of dibenzyl phosphite using methyl iodide gave Dibenzyl methyl phosphonate (9) which on lithium hydroxide hydrolysis afforded the phosphoric acid 10. Activation with thionyl chloride and subsequent reaction with Methy 4-Hydroxyphenylacetate (4) produced compound 11. Final product 12 was obtained by the catalytic hydrogenation of 11.

Compound 11 (0.060 g) was dissolved in ethyl acetate (10 ml) and 10% palladium on charcoal (0.03 g) was added. The mixture was stirred under an atmosphere of hydrogen for 3 hours. It was then filtered through a bed of celite and ethyl acetate (2 x 10 ml) added to wash products from the celite. All washings and filtrates were combined and concentrated to give compound 12 (0.038 g). This was confirmed by spectroscopy - ^1H NMR ($CDCl_3$) δ 1.48 (vbs, 3H), 3.60 (bs, 2H), 3.68 (bs, 3H), 7.15 (m, 4H), 8.20 (vbs, 1H).

Example 14

Synthesis of RT3 Substrate (see FIG. 4)

Preparation of 4-Hydroxyphenylacetamide (Compound 13)

Methyl 4-Hydroxyphenylacetate (4) (0.83 g) was dissolved in saturated methanolic ammonia (30 ml) and placed in a thick walled tube with Teflon screw cap. The solution was

stirred in this sealed tube at room temperature for 72 hours. Reaction mixture was concentrated and redissolved in methanol-chloroform (2:8 volume by volume, 75 ml). No crystallization occurred so the solution was concentrated to half its volume and hexane was added with heating.. Cooling to 0° C gave crystals of 4-Hydroxyphenylacetamide (13) (0.524 g). This was confirmed by spectroscopy - ^1H NMR (d_6 DMSO + CF_3CO_2D) δ 3.23 (s, 2H), 6.63 (d, 2H), 7.00 (d, 2H).

Preparation of Compound 15

The amide 13 was prepared by the ammonolysis of the methyl ester 4. Activation of mesitylacetic acid with thionyl chloride and subsequent reaction with amide 13 gave the final compound 15.

Mesitylacetic acid (0.10 g) was dissolved in thionyl chloride (1 ml) and stirred for 4 hours. The reaction mixture was concentrated to dryness and placed under high vacuum for 16 hours. The resultant mesitylacetylchloride (14) was dissolved in dry dichloromethane (1 ml) and added to a solution of 4-Hydroxyphenylacetamide (13) (0.076 g) and triethylamine (0.077 mL) in dry DMF (1 ml). The reaction mixture was stirred for 90 minutes then concentrated, redissolved in ethyl acetate (30 ml) and washed with saturated aqueous sodium bicarbonate (25 ml) and water (5 ml). The organic layer was dried over anhydrous $MgSO_4$, filtered and concentrated. Purification was acheived by preparative silica tlc (1 mm) using ethyl acetate as solvent to give compound 15 (0.055 g). This was confirmed by spectroscopy - ^1H NMR (d_6 DMSO + CF_3CO_2D) δ 2.13 (s, 3H), 2.23 (s, 6H), 3.35 (s, 2H), 3.83 (s, 3H), 6.80 (s, 2H), 6.93 (d, 2H), 7.23 (d, 2H).

Example 2

Hapten Conjugations

RT3 hapten, 4-(carboxymethyl) phenyl-(2,4,6-trimethylphenyl)-methyl phosphonate

(compound 7, Figure 1), was conjugated to bovine serum albumin (BSA) and keyhole limpet hemocyanin (KLH), via the free carboxyl group on the hapten.

5.4 mg of RT3 was dissolved in phosphate buffer at 37° C, and then mixed with 6 mg EDC, 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide-HCl, and N-hydroxysulfosuccciniimide (S-NHS), at a molar ratio of 1:2:2, respectively. 10 mg of BSA was dissolved in water and then added to the hapten. The molar ratio of hapten to BSA was 100:1, using a BSA molecular weight of 64,000. The mixture was stirred at room temperature for 3 hours and then dialyzed against 2 changes of phosphate buffered saline (PBS) at 4° C over 2 days.

The RT3-KLH conjugate was made in a similar manner to RT3-BSA except that the pH of the hapten, EDC, S-NHS mixture was adjusted to 6.0 with NaOH before the addition of the KLH. The hapten to protein ratio was 100:1 using a protein molecular weight of 64,000. The reaction mixture was stirred for 2 hours at room temperature, and then dialyzed against PBS at 4° C over 2 days.

After the dialysis, the protein concentrations were determined by the micro-bicinchonic acid assay using BSA as the protein standard (Pierce, Rockford, Illinois).

Example 3

Immunizations And mRNA Isolation

BALB/c female mice, 14-weeks-old, were injected intraperitoneally with 50 µg of RT3-KLH emulsified in complete Freund's adjuvant. The mice were boosted with 10 µg of RT3-KLH emulsified in incomplete Freund's adjuvant at weeks 4 and 7. The mice were sacrificed three days after the last injection and the spleen removed and used as a source of mRNA. The immune response after the second injection was measured by ELISA. The titer of the antiserum against RT3-BSA was 1:100,000.

Preparation of mRNA - mRNA was isolated from 105 mg of spleen obtained from a mouse immunized with RT3-KLH as described above. mRNA was purified using a FastTrack mRNA isolation kit (Invitrogen Corp, San Diego, CA.) following manufacturers instructions. The mRNA yield was 5.4 ug as determined spectrophotometrically using the following

formula:

$$[mRNA] = (A_{260})\ (0.04\ ug/ul)\ D$$ where D is the dilution factor

Example 4

Materials and Methods for Construction Of Phage Display Libraries

Protocols used in the following procedures were described in Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press (1989).

Restriction digestion, analysis of restriction enzyme digestion products on agarose gels, purification of DNA using phenol/chloroform, preparation of 2xTY medium and plates, preparation of tetracycline and ampicillin stock solutions, PAGE of proteins, Preparation of phosphate buffered saline, preparation of plasmid DNA by alkaline lysis, cesium chloride purification of plasmid DNA.

All enzymes were supplied by New England Biolabs (Beverly, MA) and were used according to manufacturer's instructions unless otherwise stated.

Ligations were done using an Amersham (Arlington Heights, IL) ligation kit. DNA purifications using glass milk (Bio 101, La Jolla, CA) or magic minipreps or magic PCR preps (Promega, Madison, WI) were done according to manufacturers conditions.

Preparation of competent cells and transformation were done according to the method described in the Bio-Rad (Hercules, CA) electro-transformation protocols.

The following are described in McCafferty et al., 1992, Patent No. WO92/01047: preparation of phage, phagemid particles, single stranded DNA, expression of soluble single chain Fv antibodies, the procedures for panning and ELISA, analysis of diversity by PCR and BstN1 digestion.

DNA was transformed into competent TG1 cells (genotype: K12d(lac-pro), sup E, thi, hsdD5/F'traD36, pro A+B+, Lac Iq, lac ZdM15) or HB2151 cells (genotype: K12d(lac-pro), thi/F pro A+B+, Lac IqZ dM15).

The mouse PCR primers, the vector pCANTAB 3 and pCANTAB 5, and anti-M13 antibodies are available from Pharmacia (Piscataway, NJ) (Cat. No. 27-9400-01, 27-9401-01,

27-9402-01 respectively).

Example 4.1

Preparation Of Vectors Facilitating Rapid/Multiple Isolations Of Soluble Single Chain Fv (scFv) Antibodies Using "Immobilized Metal Affinity Cchromatography Procedure" (IMAC)

In screening for catalytic antibodies, it would be advantageous to have a means of readily purifying/concentrating bacterially expressed antibodies from phagemid vectors. The following changes were incorporated into the phagemid vectors pHEN, pCANTAB (see McCafferty et al., (1992) Patent Application WO 92/01047, Hoogenboom H.R. et al., Nucl. Acid Res. 19, (1991):4133-4137, Pharmacia product literature Cat. No. 27-9401-01):

i) sequences encoding six histidine residues at the C terminus of the antibody were introduced.

ii) sequences encoding a myc tag peptide at the C terminus of the antibody were included for sensitive detection/alternative purification of SCFv's. By incorporating these changes, a very simple and rapid procedure for concentrating and purifying bacterially expressed antibodies has been developed.

Two pairs of oligonucleotides were synthesised to generate the double stranded inserts shown below. These have 5' overhangs compatible with the Not1 site and so can be cloned into this site in pHEN, pCANTAB, regenerating the Not1 site at the 5' end as shown below.

His-6 1/2

	ala	ala	his	his	his	his	his	his	amb	
5'G	GCC	GCA	CAT	CAT	CAT	CAC	CAT	CAC	TA	3'
3'		CGT	GTA	GTA	GTA	GTG	GTA	GTG	ATC CGG	5'

His-6 3/4

	ala	ala	his	his	his	his	his	his	gly	
5'G	GCC	GCA	CAT	CAT	CAT	CAC	CAT	CAC	GG	3'
3'		CGT	GTA	GTA	GTA	GTG	GTA	GTG	CCC CGG	5'

(amb= amber codon)

His-6 3/4 was cloned into pHEN-OX16 which consists of the high affinity oxazalone binding clone described in Clackson et al., Nature 352 (1991):624-628, cloned into the Pst1/Not1 site of pHEN1. This construct will give rise to a product consisting of [aOX antibody-his-6-myc tag-amber codon- gene3] which can be detected with the 9E10 antibody 9 (the cell line producing 9E10 antibody 9 is available from ATCC, Rockville, MD, CRL1729 designated MYC1-9E10.2). The new construct is called pOX16his-11 and is shown in Figure 5.

This clone was used to work out the "immobilized metal affinity chromatography procedure" (IMAC) purification regime described below. An additional construct, was made by inserting His-6 1/2 into the clone scFv4, which consists of the lysozome binding D1.3 scFv antibody cloned into pCANTAB3. This construct will give rise to a product consisting of (D1.3 antibody-his-6-amber codon- gene 3) which can be detected with anti-D1.3 antiserum.

All cloning manipulations were carried out in TG1 and the correct clones introduced into the non-suppressor strain HB2151 for expression as single chain Fvs.

All volumes are for an initial culture volume of 50 mls and all bacterial growth was at 30° C in the host HB2151. *E. coli* cells carrying the plasmid of interest were grown to 0.7-1.0 O.D./ml in 2xTY medium supplemented with 2% glucose, 100µg/ml ampicillin. The culture was centrifuged in a 50 ml Falcon tube at 3500 rpm for 10 minutes at room temperature, resuspended in 2xTY/100µg/ml ampicillin/1mM IPTG and grown for 3 hours. The culture was centrifuged in a 50 ml Falcon tube at 3500 rpm for 15 minutes at a temperature of 4° C and is resuspended in 1 ml of cold buffer A (PBS/1M NaCl/1mM EDTA) and left on ice for 15 minutes. The sample was centrifuged 2x10 minutes, the supernatant carrying the periplasmic contents collected and $MgCl_2$ added to 1-2 mM.

400 µl of a 1:1 slurry of Ni-NTA agarose:buffer 1 (Qiagen, Chatsworth, CA) which had been pre-equilibrated with buffer A was added to the periplasmic preparation and incubated for 10 minutes on an inverting platform at room temperature. The mixture was centrifuged at low speed on a microfuge for 10-15 seconds and the pellet resuspended in 1 ml of buffer A.

This process was repeated another 2 times before resuspending in 100 µl of either PBS or buffer A carrying 250 mM imidazole. After 10 minutes the supernatant was collected and the pellet re-extracted with another 100 µl of the same buffer and pooled.

Results are shown in FIG. 6, in lanes marked with the capital letters A, B, C, D, E and F. Lane A, FIG. 6 shows abundant accumulation of scFv in the periplasm after 3 hours induction. As expected scFv was only found in the culture supernatant after overnight incubation (data not shown). Isolation of antibody from the periplasm not only has the advantage that it can be prepared after a shorter induction, with the potential for a better quality product, but also the initial centrifugation step itself effectively concentrates the antibody, when working from the periplasm. Lanes B and C show that the antibody fragment is efficiently bound and recovered after incubating the Ni-NTA matrix with periplasmic extract (see Lane A) and eluting bound scFv with Buffer A/250 mM Imidazole as described above. Lanes D and E shows that elution can be carried out in PBS/250 mM imidazole, without added NaCl. This may be a more useful buffer for subsequent use of the antibody. Lane F shows that the clone scFv4his-6 produces an antibody fragment which can be recovered in the same way.

This procedure is a very simple means of concentrating/purifying antibodies which will facilitate the preparation of multiple samples simultaneously as required for screening for catalysis.

Vector forms of the above construct were prepared by cleavage with Not1 and Bam H1 to isolate DNA extending from the Not1 cloning site through to the BamH1 site in the middle of gene III. This was used to replace the equivalent Not1/BamH1 site within PCANTAB 3 and pCANTAB5 to give the vectors PCANTAB 3 his-6 and pCANTAB5 his-6. This transfers the myc tag and the his-6 tag to the new backbone (Figure 7).

Example 4.2

Preparation Of A Phage Library Derived From Mice Immunized With RT3

Sequences of all primers used for the construction, PCR and sequence analysis of mouse derived phage display libraries are shown below:

SEQUENCE OF VK PRIMARY PRIMERS.
VKA BACK 5' GAT GTT TTG ATG ACC CAA ACT CCA 3'
VKB BACK 5' GAT ATT GTG ATA ACC CAG GAT GAA 3'
VKC BACK 5' GAC ATT GTG CTA/G ACC CAG TCT CCA 3'
VKD BACK 5' GAC ATC CAG ATG ACN CAG TCT CCA 3'
VKE BACK 5' CAA ATT GTT CTC ACC CAG TCT CCA 3'
VKF BACK 5' GAA AAT GTG CTC ACC CAG TCT CCA 3'

MJK1FONX 5' CCG TTT GAT TTC CAG CTT GGT GCC 3'
MJK2FONX 5' CCG TTT TAT TTC CAG CTT GGT CCC 3'
MJK4FONX 5' CCG TTT TAT TTC CAA CTT TGT CCC 3'
MJK5FONX 5' CCG TTT CAG CTC CAG CTT GGT CCC 3'

SEQUENCE OF VH PRIMARY PRIMERS.
VH1FOR-2 5' TGA GGA GAC GGT GAC CGT GGT CCC TTG GCC CC 3'
VH1BACK 5' AGG TSM ARC TGC AGS AGT CWG G 3'

SEQUENCE OF VK LINKER PRIMERS.
VKALINKFOR
TGG AGT TTG GGT CAT CAA AAC ATC CGA TCC GCC ACC GCC AGA GCC
VKBLINKFOR
TTC ATC CTG GGT TAT CAC AAT ATC CGA TCC GCC ACC GCC AGA GCC
VKCLINKFOR
TGG AGA CTG GGT T/CAG CAC AAT GTC CGA TCC GCC ACC GCC AGA GCC
VKDLINKFOR
TGG AGA CTG XGT CAT CTG GAT GTC CGA TCC GCC ACC GCC AGA GCC
VKELINKFOR
TGG AGA CTG GGT GAG AAC AAT TTG CGA TCC GCC ACC GCC AGA GCC
VKFLINKFOR
TGG AGA CTG GGT GAG CAC ATT TTC CGA TCC GCC ACC GCC AGA GCC

SEQUENCE OF VH LINKER PRIMER.
LINK BACK 5' GGG ACC ACG GTC ACC GTC TCC TCA 3'

PULL THROUGH PRIMERS

HBKAPA10 5' CAT GAC CAC AGT GCA CAG GTS MAR CTG CAG SAG TCW GG 3'
JK1NOT10 5' GAG TCA TTC TGC GGC CGC CCG TTT GAT TTC CAG CTT GGT GCC 3'
JK2NOT10 5'GAG TCA TTC TGC GGC CGC CCG TTT TAT TTC CAG CTT GGT CCC 3'
JK4NOT10 5' GAG TCA TTC TGC GGC CGC CCG TTT TAT TTC CAA CTT TGT CCC 3'
JK5NOT10 5'GAG TCA TTC TGC GGC CGC CCG TTT CAG CTC CAG CTT GGT CCC 3'

PCR SCREEN PRIMERS
KSJ28 5'GTC ATT GTC GGC GCA ACT ATC GGT ATC 3'
FDTSEQ1 5'GTC GTC TTT CCA GAC GTT AGT 3'

Spleen mRNA was used from a mouse immunized with RT3-KLH (see Example 3) and cDNA was prepared using random hexamers (Pharmacia, Piscataway, N.J.) as primers. PCR reaction conditions are essentially as in McCafferty et al., Patent application WO 92/01047, using Taq polymerase according to manufacturers conditions.

The primary heavy chain product (VH) was made using the primer VH1FOR-2 and VH1BACK. The primary light chain PCR product (VL) was made in 5 separate reactions using an equimolar amount of the 4 MJKFONX primers with one of the 5 VKBACK primers (VKABACK, VKCBACK, VKDBACK, VKEBACK, VKFBACK). PCR conditions for VL's were 25 cycles of 94° C for 1 minute, 55° C for 1 minute and 72° C for 2 minutes, followed by a 72° C incubation for 10 minutes. For the VH's 60° C was used as the hybridization temperature rather than 55° C as this gave better results.

Linker fragments were prepared using the template pscFvNQ11 (McCafferty, J. et al., WO 92/01047) with the primer LINKBACK with 5 separate reactions each containing one of primers VKALINKFOR, VKCLINKFOR, VKDLINKFOR, VKELINKFOR, VKFLINKFOR.

Primary products were gel purified and linked together in 5 separate linkage reactions using linker fragments complementary with the 3' end of VH and with the 5' end of the various VL's. Linkage was done in a "mock" PCR reaction using the three fragments and no added primers. The linkage was carried out in duplicate in a 25 µl volume with approximately 10 ng of each fragment present. This linkage was taken through 25 temperature cycles of 94° C for 1 minute, 60° C for 2 minutes and 72° C for 2 minutes followed by a 72° C incubation for 10 minutes. 25 µl of assembly reaction was run on a gel and after de-staining the assembled product was just visible on the gel (data not shown)

The material for cloning was prepared in a secondary PCR reaction using primers which introduce cloning sites (VH1BACKAPA10 and a mix of JK1NOT10, JK2NOT10, JK4NOT10, JK5NOT10). A small amount of product from the linkage reaction was used as template (1 µl into a 50 µl PCR reaction). PCR conditions were 25 cycles of 94° C for 1 minute, 55° C for 1 minute and 72° C for 2 minutes followed by a 72° C incubation for 10 minutes.

The secondary PCR product was cut with the enzymes ApaL1/Not1, gel purified, cloned into the ApaL1 and Not1 sites of pCANTAB3his-6 and transformed into electrocompetent TG1 cells. (Transformation efficiencies were $5x10^8$/µg for pUC19 and

$1x10^6$-10^7/μg for ligated vector). A library of 1.2×10^6 clones was generated and 18/20 clones were found to have insert. Analysis by PCR and BstN1 digestion indicate that these are all different.

Example 4.3

Panning The Mouse Anti-RT3 Library Against RT3-BSA

The panning procedure was essentially as described in Marks, J. D. et al., Biotechnology 10 (1992):779-783. The RT3 hapten (compound 7, figure 1) was conjugated to BSA as described in example 2. Nunc (Kamstrup, Denmark) immunosorb tubes were coated with 1 ml of RT3-BSA at 20 mg/ml. The tubes were blocked to the top with 4 mls PBS/2% milk powder for 2 hours at 37° C and 0.8-1.0 ml of concentrated phage (equivalent to 10-50 mls of culture supernatant) was used for binding. Tubes were not inverted. Binding of phage and washing was done using MOPS buffered saline (MBS which is 50 mM MOPS pH7.4, 150 mM NaCl).

Washing was done ten times with MBS/0.1% Tween 20 and ten times with MBS. Bound phage were eluted using 800 ml of 100 mM triethylamine, neutralized with 400 ml of 1M Tris pH 7.4 and infected into exponentially growing TG1-tr cells (T phage resistant TG1 cells). The cells infected with the eluate were plated onto large (22x22cm) TY plates supplemented with 2% glucose/100 mg/ml ampicillin. Bacterial stocks were prepared next day, liquid cultures were inoculated from them and rescued with M13 helper phage and the panning procedure was repeated a second time with the concentrated phage.

The panning process was repeated and concentrated phage was used in a polyclonal ELISA. No signal was achieved from the unpanned library but increasing signal was achieved through successive pannings (not shown). The numbers of phage eluting after PAN1, PAN2 and PAN3 increased each time as expected (0.12, 50 and 2200 x 106 infectious phage respectively).

Eluted phage from PAN1 and PAN2 was introduced into HB2151 cells (a non-suppressor line producing soluble SCFv). Individual colonies were picked into 96 well

plates containing TY medium with 100 mg/ml ampicillin supplemented with 2% glucose (TY/G/A) and grown for 4-16 hours (stock plate). These cultures were used to inoculate a second 96 well plate containing TY/A and 0.1% glucose. This plate was incubated for 2-4 hours at 30° C before inducing by adding IPTG to 1 mM and growing overnight. Next day culture supernatants were added to ELISA plates previously coated with 2 mg/ml RT3-BSA and blocked with 2% milk powder. Binding was carried out in 1X MBS/2% milk powder and binding was detected using the mouse 9E10 antibody followed by goat anti-mouse-peroxidase (Sigma, St. Louis, Missouri). The 9E10 antibody used to detect the myc tag peptide is available from the ATCC, Rockville, Maryland (CRL1729, Name given is MYC1-9E10.2).

Screening for binding from PAN1 using RT3-BSA as antigen and MBS buffer throughout the procedure identified 47 positives from 364 clones. In a similar way, 115/184 positives were identified from PAN2. The diversity of the clones was analyzed by BstNI digestion of PCR amplified single chain DNA insert from each clone as described in Example 4.0.

The results are summarized in Table 1 on a group-by-group basis as shown below. 17 of 48 binders analysed from PAN1 (35%) had pattern A. A total of 78 binding clones from 115 from PAN 2 (68%) had PCR pattern A. (22 of these were restreaked and analyzed further and these are presented in the Figure 1 and Table1). Pattern B was found in 2 of 48 (4.1%) clones from PAN1 and 24 of 115 (21%) from PAN2. 2 of 48 from PAN1 had pattern C (4.1%), while 3 of 115 from PAN 2 (2.6%) had this pattern. Pattern D was found in 3 of 48 clones from PAN1 (6.2%) and 3 of 115 from PAN 2 (2.6%). Thus, the proportion of positives from each group appears to alter from PAN1 to PAN2. This could result in the loss of potentially catalytic clones after several rounds of panning if selection is based solely on strength of binding to RT3.

Table 1. Grouping Of Mouse RT3 Binders According To PCR Pattern

PCR Pattern	Sample No.
A	PAN1-3,4,6,8,9,14,17,18,24,25,27,30,35,36,45,46,47. PAN2-60,62,63,64,65,66,67,70,72,74,77,78,79,84,85,86, 87,88,91,92,96,97.
B	PAN1-12,20. PAN2-49,50,51,52,53,54,55,56,57,58,59,69,82,90,93,94, 99,100,101,102,103,104,105,106.
C	PAN1-5,48 PAN2-75,76,80.
D	PAN1-10,26,43. PAN2-68,83,89.
a	PAN1-2,13.
e	PAN1-11,19.
q	PAN1-7,15.
i (small insert)	PAN1-23,38,44.
j (small insert)	PAN1-31,40,42.
E	PAN2-71,73
10 unique patterns from PAN1	b-21, d-41, f-1, g-33, h-16, k-28, l-39, n-34, p-32, G-22.
4 unique patterns from PAN2	F-61, H-81, I-95, J-98.

At least 15 other patterns were found in PAN1 with many appearing only once. Many other patterns present in PAN1 were not identified in PAN2. In addition, some patterns

appeared in PAN2 which had not been identified in PAN1. This argues that there is much greater diversity in the library than is indicated by the PCR pattern groups which we have identified.

Example 4.4

Binding Analysis of Selected Clones from Mouse RT3 Phage Antibody Library

Several mouse RT3 phage antibody clones isolated from PAN 2 (see Table 1, Example 4.3) were characterized further in terms of binding specificity. Analysis was done using a competitive inhibition format, in which the antibody is first reacted with free hapten or product or portions of hapten and product, prior to addition to RT3-BSA coated wells as described in detail below.

The clones selected for analysis and their corresponding PCR pattern (see Table 1, Example 4.3) were: 50 (PCR B), 64 (PCR A), 68 (PCR D), 71 (PCR E), 80 (PCR C), 84 (PCR A), 95 (PCR I), 96 (PCR A), and 97 (PCR A). Soluble scFv was purified from 50 ml cultures of each clone using the IMAC protocol described in Example 4.1, except bound antibody was eluted with 50 mM EDTA, 0.5 M NaCl. The scFv concentration for each clone was estimated from silver stained SDS polyacrylamide gels by running a portion of the eluted protein on a gel containing appropriate scFv concentration standards. The scFv protein was diluted to 4 ug/ml and then serially diluted 1:2 across 11 wells of RT3-BSA coated ELISA plate. The concentration of scFv giving 50% of the maximum ELISA signal was determined from the titration. This concentration of scFv was used for a subsequent competitive inhibition assay described below.

A competitive inhibition ELISA assay was performed by incubating scFV (at a concentration as determined by titration above) with 100 uM of each of the following compounds: RT3 hapten (Compound 7, Figure 1), left hand portion of RT3 hapten (designated RT3A, Compound 8, Figure 2), right hand portion of RT3 hapten (designated RT3B, Compound 12, Figure 3), The left and right hand portions of the expected products from the esteriolytic cleavage of substrate (Compound 15, Figure 4) designated Product A

(Mesitylacetic acid, Figure 4) and Product B (Compound 13, Figure 4). The scFv was preincubated with the the inhibitor compound in tubes at room temperature for 1 hour prior to addition to RT3-BSA coated ELISA wells. The results of the assay are shown in Figure 8. The OD_{415} nm readings have been normalized to a value of 1, which represents the ELISA signal seen for the corresponding scFv in the absence of added competitive inhibitor. The results show all of the clones with the exception of 68 and 71 are inhibited in their binding to RT3-BSA with free RT3 hapten. The clones which did not show inhibition with free RT3 were shown to have cross reactivity with BSA. Clones 64, 84, 96, 97 and 50 also show binding inhibition with RT3A andto a lesser extent with Product A. No inhibition is seen for any of the clones tested with RT3B or Product B.

Example 4.5

Sequencing Of Mouse Anti-RT3 SCFv(s)

Although a large proportion of clones from PAN1 and PAN2 fall into the PCR A pattern group, it was not clear whether clones in this group were identical or diverse, and so a number of these clones were sequenced. Furthermore, in an attempt to determine whether the same heavy and light chains were being used within other major pattern groups, some representative clones from the other major groups were sequenced.

Single stranded DNA was prepared from those clones which are emboldened in Table 1 and sequencing was carried out using the Sequenase kit (USB, Cleveland, OH). Sequence alignments to Genbank germline sequences and between clones were done using the "MacVector™" (IBI, New Haven, Connecticut) program. Since the sequences at the 5' and 3' ends were encoded and enforced by PCR primers, these were "removed" for alignments. In the presentation of light chain sequences, the primer encoded sequences are not shown but the primers which were used are indicated in the right hand column. For the heavy chains, since the 5' primer is a single but degenerate primer, the sequence introduced by this primer is shown in each case. For comparison, the actual heavy chain primer sequence is shown at the 5' and 3' ends of each clone. The sequence of one clone is presented on the top line and the

differences from this sequence are indicated for the other clones. All PCR A mutations shown, which give rise to amino acid, changes were re-checked on the sequencing gels. For the heavy chains of pattern A, all unique changes were re-checked on the sequencing gel, and changes which occured in a number of clones were checked on at least one of the clones carrying that change.

Light Chain Sequences Of Mouse RT3 Binders

As shown in FIG. 9, eight different light chains have been used with the 15 different clones from pattern A. The chain associated with clones mR6 and mR8, differs from the germline V gene by a single silent nucleotide change. The chain used in mR9, mR18 and mR27 differs from mR6 and mR8 by an additional single silent mutation. Thus, these 5 clones share the same protein sequence as the germline. Clones mR9 and mR27 have used different primers to derive the same sequence, indicating that they are independant isolates of this same sequence.

Clones mR3 and mR25 are identical in the sequence which has been amplified but have also used different primers from each other. The sequence which mR3 and mR25 share in common, differs from mR6 and mR8 by 2 silent nucleotide changes and 2 changes resulting in 2 amino acid changes in FR3 and CDR3. Most changes have occurred in the light chain shared by clones 14, 30, 36, 84, and 96. In these and in all the others light chains of this group, most amino acid changes are clustered in FR3, CDR3, and FR4.

One can envisage the basic germline clone represented in mR6/8 or mR9/25, changing S to N in CDR2 and then changing in 3 different ways to give the clones represented by 4, 97 and 14 (+4 others). Similarly, there may have been a change of Y to F in CDR 3 from the same starting point, giving rise to mR3 and mR25. A third series of changes may have given rise to mR24.

The light chain associated with pattern C (clone mR80) is also shown in FIG. 9 aligned with the germline sequence used in pattern A clones. The pattern C light chain appears to be a more highly mutated form, derived from the same germline as used in pattern A.

Clones representing the other PCR patterns appear to use different germline derived sequences. The relationship of these other clones to their nearest germline is shown in FIG. 10. In pattern B (50, 69), 2 nucleotide changes from germline give rise to 1 amino acid change. In pattern D (10, 43, and 68, and 83), 8 nucleotide changes from germline give rise to 5 amino acid changes. In pattern I (95), 2 nucleotide changes from germline give rise to 1 amino acid change.

FIG. 11 shows the relationship of the different light chain sequences to that of pattern A (for mR6, 8). There is a great deal of difference between them. For patterns D and I, only the protein sequence is shown, since the nucleotide sequences have many differences. The latter two groups have longer CDR2s than the others.

Heavy Chain Sequences Of Mouse RT3 Binders

Analysis of the heavy chain sequences associated with PCR pattern A, reveals that, as for the light chain, they are all closely related but in most cases are different from each other (Figure 12). The alignment to germline is less clear in these samples. The closest germline belongs to sub-group VH-II, but there are numerous differences from this germline, in the isolated clones. In addition, there appears to be a greater number of amino acid changes between clones. As expected the changes are clustered in the CDR(s).

The heavy chains of pattern B (FIG. 13), align to a different germline and again shows numerous changes from this. All 4 clones in this group appear to be identical. Thus it appears that the clones sequenced from pattern B are multiple isolates of the same antibody. The clones represented by pattern D are all identical to each other and, excluding the sequence of CDR3, differ from the closest germline by 4 amino acids (FIG. 13).

The alignment of all the different heavy chain patterns with that of pattern B is shown in FIG. 14. The heavy chains of pattern C (80) and pattern I (95) are closely related to that of pattern B. Pattern C differs by 4 amino acids. Pattern I differs by one silent mutation and one amino acid change. Interestingly, the heavy chain associated with patterns B, C, and I has a CDR of only 3 amino acids.

The amino acid change in mR95 appears to introduce an amber codon. This would introduce an amino acid at this position when the suppressor line TG1 is used in the preparation of phage, but would be expected to act as a stop codon, in the non-suppressor line HB2151 used in the screening of soluble antibodies.

Diversity Of Clones In Pattern A

Table 2 collates the information derived from sequencing the clones in PCR pattern A. Each different light chain sequence in the group is given a label ai-aviii. Each different heavy chain sequence in the group is given a label Ai-Ax.

TABLE 2. Chain usage of mouse RT3 binders-PCR pattern A)

LIGHT CHAINS

HEAVY CHAINS	ai	aii	aiii	aiv	av	avi	avii	aviii
Ai								14,30,36, 84,96
Aii			3					
Aiii						4		
Aiv					24			
Av		9						
Avi	6,8							
Avii				64				
Aviii							97	
Aix		27						
Ax			25					

Clones 14, 30, 36 (PAN1) 84, 96 (PAN) 2 are identical and probably represent duplicate isolates of the same initial clone. Clones 6 and 8 are also identical to each other. Otherwise, every clone is different. There are two cases where the same light chain has been used with two different heavy chains (aii in mR 9/mR27 and aiii in mR3 and mR25). As described earlier, the light chains in each pairing used different primers. Apart from the duplicate isolates, there are no cases here, of the same heavy chain being used in different clones.

These PCR and sequencing experiments suggest that there is indeed a great diversity in

the mouse library both at the gross scale, as judged by PCR analysis, and at a more subtle level, as judged by sequencing.

Example 5.1

Screening of scFv Molecules for Catalytic Activity

1. Initial Selection

An early screen protocol was used to rapidly select a subset of potentially catalytic scFv molecules from the large number of scFv fragments that had been selected on the basis of hapten affinity.

a) Immobilization: The scFv fragments that bound to hapten in an ELISA assay were selected for screening to detect catalytic activity. A 96-well Millititer GV filtration plate (Millipore) was pre-wetted and washed in PBS containing 0.05% Tween-20. Suspensions of scFv fragments immobilized on anti-myc antibody Protein A agarose (vide infra, also see Example 6.1) were each transferred to separate wells in the 96 well filter plate. Residual supernatant was removed by aspiration through the filter plate. The immobilized scFv fragments were washed in the wells by filtration at 4° C with PBS/Tween (5 x 200 µL), PBS (3 x 200 µL), and 25 mM HEPES, pH 7.0, 140 mM NaCl, 0.01% NaN3 (3 x 200 µL).

b) Incubation of scFv and substrate: To immobilized washed antibody was added 200 µL of approximately 50 µM substrate (1) in 25 mM Hepes, pH 7.0,140 mM NaCl, 0.01% NaN_3 was added. Following incubation at room temperature (approximately 22° C) for approximately 24 hours after which substrate solution (but not beads) was withdrawn and frozen (-20° C) until analyzed by high performance liquid chromatography (HPLC). The same 96 well plate, still containing immobilized scFv, was washed with 4 x 200 µL/well with 10 mM Tris, pH 9.0, 140 mM NaCl, 0.01% NaN_3. Again, 200 µL of 35-50 µM of RT3 substrate (Compound 15, FIG. 4) was added, this time in the pH 9.0 buffer described above. The scFv fragments were incubated with compound 1 for 3 hours and, as at pH 7.0, substrate solution was withdrawn frozen for later analysis of product formation.

c) Analysis of Reaction Mixtures for Product Formation: To reduce the number of

samples, pools of generally two or three reaction mixtures (50 μL of each reaction mixture) were subjected to HPLC analysis. Mixtures (100 or 150 μL) were centrifuged in an Eppendorf centrifuge to prevent any carry-over of the agarose onto the HPLC system. Samples were then injected onto a Waters HPLC system equipped with a Vydac C-18 analytical reverse phase column. Components of the eluent were separated using a linear gradient over 30 minutes from 0.1% TFA in water to 0.1% TFA in acetonitrile. Product was detected and quantitated spectrophotometrically using a Waters spectral detection system, typically set at 215 or 270 nm.

Early screen analysis of 46 hapten-binding scFv fragments was carried out at pH 7.0 and 9.0 to detect catalytic activity. HPLC analysis was carried out and peak areas determined for those sample pools which gave a peak at the expected retention time for the product. The results are summarized in Table 3 below. HPLC analyses of the reaction mixtures (as pools of 2 or 3) indicated that at pH 7.0, one pool of three samples and one pool of two samples appeared to have substantial product formation. At pH 9.0 a number of pools showed product peak areas above background. Three pools of three samples showed large product peaks with peak areas greater than 0.6 and these were scored as being positive. Thus, early screen assays narrowed the number of potentially catalytic scFv fragments from 46 to 5 at pH 7.0 and from 46 to 9 at pH 9.0. Three of the candidates at pH 7.0 were the same scFv fragments as three of the candidates at pH 9.0.

TABLE 3

HPLC Assay Results of Early Screen Phage Antibody Pools at pH 7.0 and 9.0

ph 7.0

SAMPLE	PEAK AREA
BLANK	.18
1,2,3	-
4,5,6	-
8,11,12	-
14,16,17	-
18,19,20	0.52
21,24,25	-
27,28,29	-
30,31,32	-
33,34,35	-
36,37,38	-
39,40,41	-
42,44,45	0.455
46,47,48	0.476
50,65,76	0.559
83,97	0.571

ph 9.0

SAMPLE	PEAK AREA
BLANK	-
1,2,3	0.572
4,5,6	-
8,11,12	0.674
14,16,17	0.581
18,19,20	0.79
21,24,25	0.522
27,28,29	0.504
30,31,32	0.627
33,34,35	0.496
36,37,38	0.492
39,40,41	0.492
42,44,45	0.470
46,47,48	0.471
50,65,76	0.511
83,97	0.407

Individual clones from each of the active pools identified as above were reassayed for catalytic

activity. Since the scFv remains bound to the anti-Myc agarose the same material used for the pool assays was reused for the assay of the individual clones. The results of the catalytic assays are shown in Table 4 below. The catalytic assay identified 6 clones: 11, 12, 18, 19, 30, and 83, which gave a product peak on HPLC. Clone 83 was active at pH 7.0, but not pH 9.0. Clones 18 and 19 were active at both pH 7.0 and 9.0. Clones 11, 12, and 30 were active only at pH 9.0.

TABLE 4

HPLC Assay Results of Individual Page Ab Clones at pH 7.0 and 9.0

ph 7.0

SAMPLE	PEAK AREA
18 ,19	0.556
83	2.04
97	-

ph 9.0

SAMPLE	PEAK AREA
8	-
11	1.5
12	1.21
18	1.09
19	-
30	0.96
31	-
32	-

Example 5.2

1. Secondary Screening for Catalytic Activity

To further examine the scFv fragments for catalytic activity, the potentially-catalytic proteins identified in the early screen described above were individually grown and purified. Purification of the scFv was acheived as described in Example 6.1 using either IMAC or affinity chromotagraphy on anti-Myc-Protein A agarose. Assays were performed in the same buffer systems and pH values as in the early screen but the antibodies were tested individually and they were not immobilized but free in solution.

From these secondary assays, two scFv molecules, designated 18 and 83, catalytic activity was found. Clone 18 appeared to be active at pH 9.0 but not at pH 7.0 while clone 83 appeared to be active at pH 7.0 but not at pH 9.0 or 5.0. Both activities were significantly inhibited by hapten (2) when 10 μM antibody was assayed with 40 μM substrate and 30 μM

hapten. These two clones were selected as candidates for large scale purifcation of scFv as described below. The results of these assays are presented in Example 6.4.

Example 6.1

Large Scale Purification of scFv from Catalytic mRT3 Phage Antibody Clones 18 and 83

Preparation of Periplasmic Lysates-*E. coli* HB2151 clones expressing soluble anti-RT3 scFv were grown overnight in 2XYT containing 2% Glucose and 100 ug/ml ampicillin. Overnight cultures were used to inoculate 500 ml of 2XYT at a starting OD600 of 0.1 and cultures were shaken at 28° C for 3 to 5 hours until OD600 of 1.2 to 1.8. IPTG was added to 1 mM final concentration and shaking incubation was continued at 25° C for 2.5 hours. Cells were pelleted at 4,000XG for 10 minutes and pellets were resuspended in 6 ml of periplasmic lysate buffer (10 mM phosphate buffer, 1 M NaCl, 1 mM EDTA, pH 7.5. Following incubation on ice for 30 minutes, lysates were centrifuged at 6,000XG to remove cellular debris. PMSF was added to the cleared lysate at a final concentration of 5 µg/ml and lysate was stored on ice until purification as described below.

Immobilized Metal Affinity Chromotagraphy (IMAC)

$MgCl_2$ was added to the periplasmic lysate to 1 mM final concentration and lysate was passed through a 1 ml bed volume Ni^{+2} charged sepharose column (Probond Metal binding Resin, Invitrogen Corp., San Diego, CA.) washed and equilibrated with 10 mM phosphate buffer,1 M NaCl. Column was washed with 10 bed volumes of 10 mM phosphate, 1 M NaCl, pH 7.5 and bound scFv was eluted with 50 mM EDTA, 0.5 M NaCl. Column eluate was concentrated and dialyzed into 7 mM phosphate buffer, 0.15 M NaCl, pH 8.0 using a Centricon 10 microconcentrator (Amicon, Beverly, MA) following manufacturers instructions. (see Mol. Cell. Biol. 5 (1985):3610-3616). For some preperations of scFv concentration of the IMAC eluate was not required.

Anti-myc Peptide Affinity Purification- Monoclonal antibody 9E10 that recognizes a 13 amino acid peptide tag at the C-terminus of the scFV was cross-linked to Protein A agarose

using an Affinica Antibody Orientation Kit (Schleicher and Schull, Keene, NH) following manufacturers instructions. A 1 ml bed volume column was prewashed with 0.23 M Glycine, 0,3 M NaCl, pH 2.5 and reequilabrated with 10 mM Phosphate buffer, 0.5M NaCl, pH 7.5. Periplasmic lysates were diluted with an equal volume of 10 mM phosphate buffer, pH7.5 and then passed through column. Column was washed with 10 bed volumes of 10 mM phosphate buffer, 0.5M NaCl and bound scFv was eluted with 0.23M glycine, pH2.5, 0.3M NaCl. For some preperations the column eluate was dialyzed and concentrated using a Centricon 10 microconcentrator as described above.

Example 6.2

Purification Of ScFv Fragments from Phage Antibody Catalytic Clones 18 and 83 By Hydrophobic Interaction Chromatography

Following IMAC or anti-myc peptide Protein A agarose purification of scFv derived from lysates of *E. coli* clones 18 and 83 (see Example 6.1), further purification of the scFv was accomplished on an alkyl superose 5/5 column attached to an FPLC system (Pharmacia).

Chromatography was performed using a linear reverse gradient of $(NH_4)_2SO_4$ in 0.1 M Na phosphate pH 7.0. This was formed from two buffers:

Buffer A: 2M $(NH_4)_2SO_4$ in 0.1 M Na phosphate pH 7.0

Buffer B: 0.1 M Na phosphate pH 7.0

Gradient conditions were:

0 - 3 ml:	10% Buffer B
3 - 39 ml:	Linear gradient, 10% - 70% Buffer B
39 - 42 ml:	Linear gradient, 70% - 100% Buffer B
42 - 44 ml:	100% Buffer B
44 - 46 ml:	Linear gradient, 100% - 10% Buffer B
46 - 49 ml:	10% Buffer B

Samples were adjusted to a final concentration of 1.8 M $(NH_4)_2SO_4$ by the addition of 0.783 vols of a saturated solution of $(NH_4)_2SO_4$ in 0.1 M Na phosphate (4.1 M $(NH_4)_2SO_4$) and dilution with an appropriate volume of 10% Buffer B: 90% Buffer A to increase the volume to a value suitable for injection onto the column. Fractions were collected and the peak(s) corresponding to ScFv identified by SDS PAGE as described below. These were pooled, concentrated and used in assays for binding or catalytic activity as appropriate.

Elution of protein from the column was monitored by OD_{280} and plotted automatically. A typical chromatogram for IMAC pure scFv from clone 18 shows the bulk of the protein elutes in two distinct peaks. Fractions corresponding to each of the peaks were pooled as indicated. Peak 1 consisits of a broad shoulder eluting at 17.25 to 21.90% Buffer B (Pool 1) followed by a sharp peak at 24.2% Buffer B (Pool 2). Peak 2 is a sharp peak eluting at 48.10% buffer B (Pool 3). Purification of the scFv was monitored by silver stained SDS/PAGE with the following results. Load material for the HIC column (IMAC pure scFv + $(NH_4)_2SO_4$) showed >90% of the protein was scFv. At least four additional bands were also visible. Analysis of Pool 1 and Pool 2 obtained following HIC showed the majority of the scFv that was loaded was distributed equally in these pools and no substantial purification of the scFv was acheived. Pool 3 contained a small amount of scFv and an additional low molecular weight band.

The chromatogram for clone 83 shows the bulk of the scFv protein elutes in a single sharp peak at 54.7% Buffer B. A second minor peak of protein elutes during the final wash with 100% Buffer B. Fractions corresponding to these peaks were pooled and analyzed by SDS/PAGE followed by silver staining. The column load material for HIC (IMAC purified material + $(NH_4)_2SO_4$) contained >90% scFv. After HIC the majority of the scFv is recovered in the single main peak eluting at 54.7% Buffer B. As with clone 18, no substantial purification of the scFv was acheived by HIC. A small amount of scFv is found in the late eluting minor peak.

Example 6.3

Binding Assays of IMAC and HIC Pure scFv from Phage Antibody Catalytic Clones 18 and 83

Fractions or pools of fractions from the purification protocols described above (see Example 6.1 or 6.2) were analyzed for RT3 binding activity using an RT3-BSA solid phase ELISA assay essentially as described in example 4.4. The fraction or fraction pools were first diluted 1:5 or 1:10 in PBS/Tween-20 and then serially diluted 1:2 with PBS/Tween-20 across 11 wells of the RT3-BSA coated ELISA plate. The titer which gave the 50% maximal ELISA signal was determined for each sample analyzed. By multiplying this titer by the volume of the pool or fraction analyzed, an estimate of the number of binding units in each sample could be determined. This analysis showed that for clone 83 even though majority of the scFv loaded on the HIC column was recovered it had less than 10% of the binding activity compared to the column load. This result suggests that HIC may be unsuitable for purification of the scFv, since it may result in perturbations of the scFv protein structure resulting in loss of binding and presumably catalytic activity.

Example 6.4

Catalytic Assays of IMAC and HIC Purified scFv from Phage Antibody Clones 18 and 83

For clone 18 a typical catalytic assay was set up as follows: 50 µl of scFv was added to 145 µl of RT3 substrate (Compound 15, FIG. 4) and 5 µl of water or for some assays 5µl of RT3 hapten. A blank consisting of 50 µl of water and 147 µl of RT3 substrate was set up to monitor the background hydrolysis of the RT3 substrate. The reaction was allowed to proceed for 6 hours after which samples were frozen at -20° C to stop the reaction. Samples were analyzed by HPLC as described in example 5.1. The amount of scFv added to an assay typically ranged from 1 to 5 ug and protein was buffered in 10 mM Hepes, 150 mM NaCl, pH 7.3. The typical RT3 substrate concentration was 50 uM buffered in 25 mM Tris-Cl, pH 9.0, 140 mM NacL and 0.01% NaN_3.

An HPLC profile showing a typical positive catalytic assay result for IMAC pure 18 scFv is shown in Figure 15A. Figure 15B shows the HPLC profile of the same assay but done in the presence of RT3 hapten (Compound 5, FIG. 1). Finally, Figure 15C shows the HPLC profile of the blank (no added scFv).

In a similar manner assays of the fraction pools obtained following HIC purification of 18 scFv (see Example 6.2) were also performed. A typical result for the assay of the main scFv-containing pool (Pool 2 as described in Example 6.2 above) is shown in Figure 16. Similar results were obtained from assays of Pool 1 and Pool 3 (data not shown).

Assay of IMAC or HIC purified scFv from clone 83 was done in a similar manner as described for clone 18 with the following exceptions. Substrate was buffered in 25 mM HEPES, pH 7.0, 140 mM NaCl and 0.01% NaN_3. Due to the lower background hydrolysis of RT3 substrate at neutral pH, reactions were typically run for 24 hours. An HPLC profile of a positive catalytic assay result for IMAC pure 83 scFv is shown in Figure 17A. The same assay repeated in the presence of RT3 hapten is shown in Figure 17B. A blank was also analyzed and gives a profile similar to the that in Figure 17B (data not shown). A catalytic assay of the main scFv containing pool obtained following HIC (see Example 6.2) is shown in Figure 18.

It should be noted that the retention times of the expected product peak as well as non-product related peaks varied from run to run on the HPLC. The reason for this variation is not known. Test runs of the RT3 product (Compound 13, FIG. 4) alone on HPLC and monitoring at 215 nM showed a distinct peak profile was produced. This 215 nM profile was used as an internal control to accurately determine the position of the product peak on the 270 nM profile for each HPLC run.

Conclusions from the results of the catalytic assays performed as described above are as follows. IMAC pure scFv from both clone 18 and 83 is able to hydrolyze the RT3 substrate and produces a product peak that elutes from the HPLC column at the correct retention time. In the presence of RT3 hapten, catalysis is completely abrogated presumably due to the much tighter binding of the RT3 hapten in the antibody pocket compared to the RT3 substrate. This

is further evidence that the scFv is responsible for catalysis since it is unlikely that natural esterase exists which is capable of specifically recognizing and binding the RT3 substrate or hapten with high affinity.

Following HIC purification of scFv for either clone 18 or 83 no catalytic activity was observed in the scFv containing fractions. Loss of activity could possibly be due to instability of the scFv resulting in unfolding or aggregation. Instability of the scFv for clone 83 was clearly demonstrated by the loss of binding in the assays performed on HIC purified scFv as described in Example 6.3

Example 7.1

Isolation Of Binders To The Transition State Analogue, RT3 From A Naive Human Library

It has been demonstrated that immunization schemes can be by-passed and that low and moderate affinity human antibodies (Kds down to 86 nM) can be isolated directly from human antibody libraries derived from non-immunized sources (Marks et al., J. Mol. Biol. 222 (1991):581-597). This approach could provide a starting clone (or clones) which could be improved by a number of approaches as described by example below (for related examples see Marks et al., BioTechnology 10 (1992):779-783). These approaches could, therefore, lead to the isolation of entirely human catalytic antibodies which could prove extremely valuable, particularly in the area of therapeutic catalytic antibodies.

The non-immunized human library described in Marks et al., J. Mol.. Biol. 222 (1991):581-597, was panned against RT3-BSA, coated onto tubes as described for the immunized mouse library except 100-200 µg/ml RT3-BSA coating concentration was used. The progress of the purification schemes was monitored by ELISA(s) using polyclonal phage. Polyclonal phage derived from 2 rounds of panning against RT3-BSA (RT3BSA:2) gives a signal which is visible after overnight incubation with substrate. Polyclonal phage derived from 3 rounds of panning against RT3-BSA (RT3BSA:3) gives a strong signal on ELISA (1 O.D. in 5 minutes). No binding to BSA was observed and binding to RT3-BSA was inhibited by pre-incubation with 10-100 µg/ml of soluble, unconjugated RT3 suggesting that it was specific

for RT3 (not shown).

Individual clones derived from 3 and 4 rounds of panning were examined for binding using methods as described in example 4.3. Before beginning to screen on a large scale, the minimum ELISA coating concentration was determined. Reducing antigen concentration from 100 µg/ml to 1.6 µg/ml (100 µl/well) causes only a 30% reduction in signal (data not shown) 2 µg/ml concentration was, therefore, used in all subsequent ELISA screenings

144 clones derived from 3 rounds of panning were examined by ELISA assay for specific binding to RT3-BSA using 100 µl of culture supernatant from IPTG induced HB2151 clones. As shown in FIG. 19A , 40 clones gave strong ELISA signals (0.7 to 2.5 O.D. after overnight incubation with substrate) and 27 gave moderate signals (0.2-0.5 O.D. after overnight incubation with substrate). FIG. 19B shows the results for 48 clones derived from 4 rounds of panning against RT3-BSA. From this 39 clones showed strong ELISA signal (0.7-2.5 O.D.) and 1 moderate ELISA signal (0.34 O.D.).

PCR analysis and Bst N1 digestion revealed that all the the good binders examined from both rounds of panning shared a common PCR pattern and all but one of the weaker binders examined shared a common PCR pattern which is different to that of the high binders. One additional pattern was found associated with one of the weak binders. It is interesting to see enrichment with successive rounds of panning of the clone associated with high ELISA signal relative to that for moderate signal, as previously described by Clackson et al., Nature 352 (1991):624-628.

Example 7.2

Sequence Analysis Of Human RT3 Binders

Sequencing was carried out on various members of each PCR pattern group as shown below:

PCR1= RT3:1, 4, 5, 41, 63, 80.
PCR2= RT3:47, 54
PCR3= RT3:61

nucleotide and deduced amino acid sequences of each group FIG. 20.

Example 8.1

Chain Shuffling Of Human RT3 Binders

The scheme used for chain shuffling is shown in FIG. 21. All of the scFv clones in the human or mouse libraries share certain common sequences including the plasmid sequences upstream of the heavy chain, the linker sequences between the heavy and light chains and gene 3 sequences downstream of the light chain. Primers were selected/synthesized from these areas to provide a general means of ampifying cloned heavy or light chain V regions. Thus, PCR using the primers LMB3 and PCRHLINK will give rise to a heavy chain product while the primers FDTSEQ1 and LINKPCRL will give rise to a light chain product. LINKPCRL and PCRHLINK are complementary and so provide a means of linking the products. In this way, the separate heavy or light chains from each clone can be linked to a whole population of complementary chains derived from the initial library. The linked product acts as a template for a secondary PCR using the primers LMB3 and FDTSEQ1 and the secondary product is digested with Sfi1 and Not1 for cloning. The primers were chosen to enable a change in fragment size to be observed following each digestion step. In addition, the efficiency of digestion is probably improved by having a relatively large overhang upstream of the restriction site.

Method For Chain Shuffling

The following primers are used:

FDTSEQ1	5'GTC GTC TTT CCA GAC GTT AGT 3'
LMB3	5'CAG GAA ACA GCT ATG AC 3'
PCRHLINK	5'ACC GCC AGA GCC ACC TCC GCC 3'
LINKPCRL	5'GGC GGA GGT GGC TCT GGC GGT 3'

Primary heavy and light chain PCR products are prepared in the following reactions:

HEAVY		LIGHT	
LMB3 primer (10pmoles/ml)	2.5µl	FDTSEQ1 primer (10pmoles/ml)	2.5µl
PCRHLINK primer (10pmoles/ml)	2.5µl	LINKPCRL primer (10pmoles/ml)	2.5µl
10X PCR reaction buffer	5.0µl	10X PCR reaction buffer	5.0µl
5mM each dNTP's	2.5µl	5mM each dNTP's	2.5µl
Taq polmerase (5U/ml)	0.3µl	Taq polymerase (5U/ml)	0.3µl
water	37µl	water	37µl

PCR conditions are 25 cycles of 94° C 1 minute, 60° C 1 minute, 72° C 2 minutes with a final 10 minutes at 72° C. For isolated clones template can be most simply provided as a toothpick innoculum from a bacterial colony. For library material, DNA was prepared from a frozen bacterial stock and 2-10 ng added to the reaction. Primary PCR products were purified on agarose gels and purified using 5 µl of Geneclean "glass milk" (Bio 101, La Jolla, CA) with two elutions in water of 10 µl each.

Assembly is carried out as follows:

purified heavy	2.5 µl (20-50 ng)
purified light	2.5 µl (20-50 ng)
10X reaction buffer	2 µl
5mM each dNTP(s)	1.0 µl
Taq polymerase	0.2 µl
water	37 µl

PCR conditions are 25 cycles of 94° C 1 minute, 65° C for 4 minutes with a final 10 minutes at 72° C.

For secondary PCRs, 1 µl of the linked material was used as template. The reaction was set-up as follows:

linked PCR product	1 µl
LMB3 primer (10pmoles/ml)	2.5 µl
FDTSEQ1 primer (10pmoles/ml)	2.5 µl
10X PCR	

reaction buffer	5.0 µl
5mM each dNTP(s)	2.5 µl
Taq polmerase (5U/ml)	0.3 µl
water	37 µl

PCR conditions are 25 cycles of 94° C 1 minute, 60° C 1 minute, 72° C 2 minutes with a final 10 minutes at 72° C (5 µl can easily be seen on a gel).

The secondary product was extracted with phenol:chloroform and precipitated with ethanol, to remove Taq polymerase. The PCR product was digested overnight at 50° C with Sfi1 according to manufacturers instructions. Next day 1/10th volume of 1M NaCl was added to give a final concentration of 150 mM NaCl and Triton-X100 added to a final concentration of 0.01% before digesting with Not1 for 3 hours at 37° C. The digest was treated with phenol:chloroform, precipitated, dissolved in H_2O and purified by running on a 1.5% agarose gel and purified with "Geneclean"(Bio 101, La Jolla , CA). The DNA was eluted into a final volume of 10-15 µl and cloned into the Sfi1/Not1 site of pCANTAB5 his-6.

Plasmid DNA of pCANTAB5 his-6 was prepared by the alkaline lysis method and was purified by cesium chloride centrifugation. The purified DNA was digested at a DNA concentration of 100 µg/ml with Sfi1 according to manufacturers instructions (50° C for Sfi1, overnight) followed by a 3 hour digestion with Not1. The digestion product was loaded on directly on to a Chromaspin 1000 column (Clontech, Palo Alto, CA) to remove the stuffer fragment and spun for 3 minutes at 2200 rpm in a bench top centrifuge. The DNA was then phenol:chloroform extracted and dissolved at 100 µg/ml for use.

Ligations are carried out using an Amersham (Arlington Heights, IL) ligation kit as follows:

Vector DNA	1 µl(100 ng)
insert DNA	2 µl (10-50 ng)
10 mMMgCl, 200 mM Tris pH7.4	3 µl
buffer A	24 µl
buffer B	6 µl

Incubate for 30-60 minutes at 16° C. For library preparation, 5 times the volumes shown above were used. The ligation product was concentrated and purified using Geneclean and eluted into a volume of 10-15 µl of water. This was introduced into electrocompetent T phage resistant TG1 cells using a Bio-Rad (Hercules, CA) electroporator, according to manufacturers instructions.

Three clones, hRT3-1, hRT3-47, and hRT3-61 isolated after four rounds of panning of the naive human library (see Example 5.1) were used as templates for the chain shuffling protcol described above. As described in Example 5.2, sequence analysis showed each of the three clones were unique from each other in terms of VH and VL gene usage. Six different libraries were prepared. In each case, the name of the library refers to the fixed chain and the clone number from which it was derived. Thus, H47 is a library with a fixed heavy chain from RT3:47 combined with a library of human light chains.

The library sizes obtained were as follows:

TABLE 3

Library	Size(X 10^6)	Proportion with insert
H1	7.8	9/10
H47	6.2	8/10
H61	6.8	9/10
L1	9.6	9/10
L47	9.8	9/10
L61	8.4	8/10

PCR using the primers FDTSEQ1 and LMB3 was carried out on 10 colonies from each library to determine the proportion with insert. The results are shown in the table above. In addition the PCR products were digested with BstN1 to determine the diversity. It should be remembered, however, that approximately 2/3 of the sequence (of any given clone) in the chain shuffled library, is now fixed and that different members of the same V gene family may give the same "BstN1 signature". Despite this, none of the library members had the pattern associated with the original clone. In some cases, patterns were found in duplicate within some libraries and one pattern may have appeared 3 times in the H1 library.

Example 8.2

Panning Human Chain Shuffled Library

Phage particles were rescued from the libraries as described in Marks et. al., Biotechnology 10 (1992):779-783. Phage from pairs of libraries derived from the same starting clone were pooled and panned against RT3-BSA (e.g., H1 and L1). Panning and rescue were done essentially as described in Marks et al., J. Mol. Biol. 222 (1991):581-597). except Nunc (Kamstrup, Denmark) immunosorb tubes were coated overnight with 1 ml of RT3-BSA at 20 µg/ml. Coating and blocking were done in phosphate buffered saline (PBS) as before. The equivalent of 20 mls of phage was used in a final volume of 800 µl of MOPS buffered saline (MBS) with 2% dried milk powder. Washing, elution, infection, and rescue with M13 helper phage were as described above.

"Polyclonal" phage derived from either the unpanned libraries (PAN0), from the first round of panning (PAN1), or from 2 rounds of panning (PAN2) were used in an ELISA to determine the progress of the panning process for each pair of libraries.

As shown in FIG. 18, no signal was observed from PAN0 samples. Low level signal is observed in PAN1 samples derived from RT3:1 and RT3:47 and there is a marked improvement in PAN2 samples. With libraries derived from RT3:61, ELISA signal is still relatively low after two rounds of panning. The ELISA results are mirrored when the eluate from each round of panning is quantitated as shown in Table 4. Increasing numbers of phage are eluted from the second panning. The numbers of phage yielded from PAN1 and PAN2 on the H61/L61 libraries is lower than the corresponding yield from H1/L1 and H47/L47 libraries.

TABLE 4

Yield of phage from pannings (X106)

	shuffled RT3:1	shuffled RT3:47	shuffled RT3:61
eluate of PAN1	1.4	2.9	0.34
eluate of PAN2	1300	1600	200

input phage approximately 2-10 X 1012

Table 5 shows the proportion of positives derived from panning the reshuffled human binders. For reshuffled RT3:1 and RT3:47, even after one round of panning the majority scored positive. Since polyclonal phage from reshuffled RT3:61 was negative after PAN1, and positive after PAN2, individual colonies were only analyzed from PAN2 from this library.

Table 5 Proportion Of Positives From Reshuffled Human Libraries

POPULATION	PROPORTION POSITIVE	NUMBERS RESTREAKED
RT3:1 Reshuffle		
PAN1	39/44	28
PAN2	42/44	15
RT3:47 Reshuffle		
PAN1	29/44	25
PAN2	35/48	28
RT3:61 Reshuffle		
PAN2	44/96	37

Positive clones were restreaked and retested for RT3 and BSA binding. All reshuffled human libraries gave rise to a high proportion of binders after 1-2 rounds of panning. These have been grouped by PCR/BstN1 digestion (using FTDSEQ1 and LMB3) into 9 PCR pattern groups for the RT3:1 reshuffled library, 4 PCR pattern groups for the RT3:47 reshuffled library and 8 PCR pattern groups for the RT3:61 reshuffled library as shown in Table 6 below.

There is a strong possibility that a heavy chain shuffled, with a library of light chains, will pull out different light chains, which are related to each other, and so the potential for PCR pattern diversity is reduced. Conversely, it is likely that a degree of diversity will be found by sequencing, even within a given PCR grouping.

Table 6. Grouping Of Human RT3 Binders According To PCR

A. RESHUFFLED CLONES ARISING FROM HU RT3:1

PCR Pattern	Sample No.
A	PAN1-1, 5, 6, 9, [10], 12, 21, 27. PAN2-31, 34, 35, 36, [38], 41, 42, 43.
B	PAN1-2, 3, 4, 8, 11, 13, 22, 24 [25]. PAN2-30, 39.
C	PAN1-[7], 14, [15], [19], 23. PAN2-29, 33.
D	PAN1-17, [18], [26]. PAN2-[44].
E	PAN2-32, 40.
F	PAN1-[20].
G	PAN1-28.
H	PAN1-16.
I	PAN1-37.

3/ All samples from RT3:1 were negative for BSA binding apart from a very low level in sa

B. RESHUFFLED CLONE ARISING FROM HU RT3:47

PCR Pattern	Sample No.
A	PAN1-2, 4, 12,17,20,21,22. PAN2-4, 5, 6, 7, 27, 28, 29, 31, 33, 40, 41, 42, 44, 48, 49,51, 52, 53.
B	PAN1-9, 10.
C	PAN1-1. PAN2-37.
D	PAN1-3, [26].
Pattern Unknown	Negative on re-screening PAN1-13, 14, 15, 16, 18, 19, 23, 24, 25. PAN2-30, 32, 34, 35, 36, 38, 39, 43, 45, 46, 47, 50. Binder to BSA PAN1-11

C. RESHUFFLED CLONE ARISING FROM HU RT3:61

PCR Pattern	Sample No.
A	PAN2-2, 8, 10, 11, 13, 14, 15, 17, 18, 20, 21, 23, 24, 25, 26, 28, 29, 32, 34, 35.
B	PAN2-16, 30, 33.
C	PAN2-4.
D	PAN2-6.
E	PAN2-12.
F	PAN2-9.
G	PAN2-22.
H	PAN2-31.
Pattern Unknown	Negative on re-screening. PAN2-1, 3, 5, 27, 36, 37. Positive on re-screening. PAN2-7. Binder to BSA. PAN2-19.

Foomote:
1/ Samples are all labelled hu(original clone number)-reshuffled clone number e.g. hu 47:12 human clone derived from chain shuffling clone RT3:47 from the first panning and numbering derivative 12. For presentation here, only the clone number is given.
2/ The use of the same letters for pattern groups derived from different starting clones, is not meant to imply that they are the same.
3/ Samples in brackets had been scored positive first time round but the clones picked after restreaking did not come up positive. This is either due to mixed colonies in the original were variable expression from different preparation or initial false positives. Sequencing was carried out on a number of clones derived from huRT3:47 and these are emboldened in Section B.

In an attempt to determine which antibody chain was derived from the original human clone, separate PCR of the heavy and light V genes was carried out on individual clones (using either FDTSEQ1 or LMB3 in conjunction with primers located in the sequence encoding the

flexible linker peptide between the chains (PCRHLINK and LINKPCRL). Pairs of clones from each PCR group were analyzed (underlined in Table 6). This result indicates that all heavy chains, with the exception of hu61:16 and hu61:33 (pattern B) had the same heavy chain as the original isolate. These two clones now have a heavy chain pattern similar to RT3:47 and a light chain pattern which may be similar to the parent clone, RT3:61. Reshuffled clones which had been described as having the same PCR pattern (from PCR/digest of whole SCFv, run on 3% gel) now show subtle differences (from PCR/digest of individual light chains, run on 4% gel). Thus, differences were found between hu1:11 and hu1:22 (pattern B), hu1:17 and hu1:26 (pattern D), hu1:32 and hu1:40 (pattern E). For clones derived from RT3:47, differences were found between light chains of hu47:9 and hu47:10 (pattern B), hu47:37 and hu47:1 (pattern C). For clones derived from RT3:61, differences were found between light chains of hu61:13 and hu61:24 (pattern A). This analysis, therefore, reveals even greater diversity between the clones.

Sequencing was carried out on clones derived by shuffling RT3:47. (emboldened in Table 5). Analysis of the heavy chains shows that with the exception of hu47:7, the sequence is identical to the original heavy chain. (Clones analysed were hu47:1, 2, 3, 5, 6, 8, 9, 10, 12, 20, and 22.). In hu47:7 a valine in CDR2 is converted to an alanine by a T to C change. Sequencing of the light chain was carried out on the clones underlined in Table 5.

Example 9.0

Directed Selection Using Specific Elution/ Competitive Binding

It is hoped that panning procedures using competition for binding (e.g., with reaction products) or specific elution (e.g., with smaller phosphonates) can be used to control the panning process. A greater degree of flexibility could be exerted if such procedures were carried out in ELISA wells. Thus, following a particular procedure, the eluate could be collected and the whole plate carried through a detection procedure. Based on the results, the eluate from specific wells could be selected for further analysis/pannings.

In an experiment to examine the elution from 96 well plates using 100 mM

triethylamine, it was found that the overnight ELISA signal following elution, went from 0.289 to 0.019. (Using 2.5 X 10^{11} polyclonal phage/well derived from one round of panning the shuffled human RT3:47 library (47PAN1 phage). Titration of the eluate showed that 7.5X 10^7 infectious phage were collected, i.e., 0.03% of input. This compares favorably with elution from Nunc immunosorb tubes where 1.6X 10^9 infectious phage were yielded from an input of 1X 10^{13} for the same sample, i.e., 0.016% (see Table 3). By this type of approach, a range of specific elution procedures could be compared and the most suitable samples infected into *E. coli* for further work.

The minimal transition state analogues, equivalent to the left and right hand of the RT3 molecule, will be referred to as RT3a (Compound 8, FIG. 2) and RT3b (Compound 12, FIG. 3). The left and right hand products of substrate cleavage will be referred to as product A (Mesitylacetic acid, FIG. 4) and product B (Compound 13, FIG. 4). In order to determine the optimal concentrations of the various components required for panning/elution of the original mouse library, a dilution series was prepared for RT3, RT3a, RT3b, and both reaction products (product A and product B). These were pre-incubated with 100 µl of 10x polyclonal phage derived from one round of panning the mouse RT3 library (using triethylamine elution).

The results of this analysis are presented in FIG. 23A and 23B. The most effective inhibition occurs with RT3 itself. It is clear that binding of this selected phage population is inhibited to a far greater extent by the left hand TSA and product (FIG. 23A) than by the right hand portions (FIG. 23B). Indeed, it is not at all clear if any inhibition occurs at the concentrations tested with right hand TSA or product. Furthermore, it appears that there is greater inhibition by the left hand TSA than the left hand product.

Specific elution was attempted using the original unpanned mouse library. This was carried out by binding 200 µl of 10x phage concentrate to ELISA wells coated with 150 µl of 2 µg/ml RT3-BSA and blocked with 200 µl of 2% Marvel. Phage were allowed to bind for 1 hour and were eluted by adding 200 µl of the following:

0.05 μM, 0.5 μM or 5 μM RT3

5 μM, 50 μM or 500 μM RT3a

5 μM, 50 μM or 500 μM RT3b

100 mM triethylamine

Phage derived from two 15 minute elutions were pooled and reintroduced into TG1 or HB2151 cells. FIG. 24A plots the yield of phage under each set of conditions. Triethylamine gives approximately 10^4 phage from an input equivalent to 2 ml of culture supernatant. This is in line with the successful panning described in the previous report, which has given rise to all the mouse clones described earlier. In that experiment, approximately 10^5 phage were derived from an input, equivalent to 20 ml of culture supernatant. Elution with RT3 and RT3a gives rise to a greater number of phage than triethylamine. RT3b gives a level of elution equivalent to or just greater than that achieved in a "buffer only" control.

This experiment was repeated, but a higher coating concentration of RT3-BSA was used (100 μg/ml), and volumes were adjusted to ensure that coating and blocking volumes exceeded the volume of input phage (to prevent any background problems associated with non-specific sticking of phage up the side of the well). In this experiment (Figure 24B), the overall yield of eluted phage in all samples was reduced from before.

Polyclonal phage and soluble antibody was prepared from the various populations and tested in ELISA. Positive signals were achieved with soluble and phage ELISA, from sample derived by elution with 500 μM RT3a where. Individual colonies from this population were screened and 22/144 of the clones were found to be positive.

Panning was also carried out in the original immunosorb tubes (Nunc). Elution was carried out using either 100 mM triethylamine or 500 μM RT3a. Binding was carried out in the presence or absence of product A. (50, 500, 5000 μM). The results are summarized below:

ELUTION REGIME	CONCENTRATION OF COMPETING PRODUCT	YIELD ($X10^6$)
1/ 100 mM triethylamine	0 μM product a	52
2/ 500 μM RT3a	0 μM product a	42
3/ 500 μM RT3a	50 μM product a	0.59
4/ 500 μM RT3a	500 μM product a	0.85
5/ 500 μM RT3a	5000 μM product a	47

In this experiment, the yield of phage by triethylamine and RT3a elution (42-52 $x10^6$) is higher than previous experiments. The yield of phage from RT3a elution is reduced by 70 fold when 50 μM product A is present during binding (suggesting binding is specific). There is a similar reduction with 500 μM product A, but when 5000 μM product A is used, the yield returns to 47 x 10^6. (This may be an effect of DMS, used to dissolve the product, which was present at 7.2% in this particular sample). Thus, it is possible to elute phage from either 96 well plates or immunosorb tubes using hapten elution with minimal TSA molecules. Furthermore, the binding profile may be altered by competing with reaction products, thereby tailoring the binding profile of the eluted population according to the desired requirements.

Example 10

CDR Shuffling Of Human RT3 Binders

The scheme used for shuffling CDR fragments is a modification of the chain shuffling scheme described in Example 8.1.

The primers VHCDR3BACK and REV VHCDR3BACK are complementary to each other and to a conserved sequence in the framework region of human VH genes immediately upstream of CDR3. A population of DNA fragments which includes both CDR1 and CDR2 of the heavy chain from the library described by Marks et al., (1991) can be amplified using REV VHCDR3BACK (see below for sequence) and LBM3 (described in Example 4.2) and the remainder of the scFV from the chosen clone can be amplified using VHCDR3BACK (see below for sequence) and FDTSEQ1 (described in Example 4.2). This permits the linkage of a population of CDRs 1 and 2 with the remaining portion of a single clone by a two-fragment

assembly reaction.

Similarly, a library of DNA fragments containing the CDR3 region of the heavy chain may be amplified using VHCDR3BACK and the linker located primer, PCRHLINK (see example 4.2). The remaining portion of the heavy chain from the chosen clone was amplified with REV VHCDR3BACK and LMB3 and the light chain was amplified with LINKPCRL (see example 4.2) and FDTSEQ1. Thus, a population of CDR3 fragments may be introduced into a single clone by two sequential two-fragment assembly reactions; the first invovling assembly of CDR 1 and 2 from the clone with the population of CDR3s. This is followed by a secondary PCR reaction using the flanking primers of this fragment LMB3 and PCRHLINK. the product of this was gel purified for subsequent assembly of this with the light chain from the clone.

For both CDR shuffling regimes, a final PCR reaction using the scFV-flanking primers LMB3 and FDTSEQ1 is performed. The CDR shuffled material is then digested with Not1 and Sfi1 for cloning into pCANTAB5-his 6 (see FIG. 7).

Method For CDR Shuffling

The primers FDTSEQ1, LMB3, PCRHLINK and LINKPCRL are described in Example 4.2. In addition, the following primers are used:

VHCDR3BACK 5' GAC ACG GC(TC) GT(AG) TAT TAC TGT 3'
REV VHCDR3BACK 5' ACA GTA ATA (CT)AG (GA)GC CGT GTC 3'

(Nucleotides in paraentheses indicate introduced "wobbles" in the primer design to ensure universal amplification.)

Primary PCR products are prepared in the following reactions:

CD 1 and 2 Fragment	
LBM3 primer (10pmoles/µl)	2.5 µl
REV VHCDR3BACK primer (10 pmoles/µl)	2.5 µl
10X PCR Reaction Buffer	5.0 µl

5 mM each dNTP(S)	2.5 µl
Taq polymerase (5U/µl)	0.3 µl
Water	to 50 µl

CDR3 Fragment

PCRHLINK primer (10pmoles/µl)	2.5 µl
VHCDR3BACK primer (10pmolesµl)	2.5 µl
10X PCR Reaction Buffer	5.0 µl
5 mM each dNTP(s)	2.5 µl
Taq polymerase (5U/µl)	0.3 µl
Water	to 50 µl

VHCDR3-Linker-VL Fragment

FDTSEQ1 primer (10pmoles/µl)	2.5 µl
VHCDR3BACK primer (10pmolesµl)	2.5 µl
10X PCR Reaction Buffer	5.0 µl
5 mM each dNTP(s)	2.5 µl
Taq polymerase (5U/µl)	0.3 µl
Water	to 50 µl

Linker-VL Fragment

FDTSEQ1 primer (10pmoles/µl)	2.5 µl
LINKPCRL primer (10pmolesµl)	2.5 µl
10X PCR Reaction Buffer	5.0 µl
5 mM each dNTP(s)	2.5 µl
Taq polymerase (5U/µl)	0.3 µl
Water	to 50 µl

Miniprep DNA was prepared from the library described by Marks et al. (1991) as template for PCR. PCR produced from the clone was prepared by innoculating from a bacterial colony.

PCR conditions were 25 cycles of 94° C 1 minute, 55° C 1 minute, 72° C 2 minutes with a final 10 minutes at 72° C.

Primary PCR products were gel purified using the Promega Magic PCR Prep System

5 mM each dNTP(S)		2.5 µl
Taq polymerase (5U/µl)		0.3 µl
Water	to 50 µl	

CDR3 Fragment

PCRILINK primer (10pmoles/µl)		2.5 µl
VIICDR3BACK primer (10pmolesµl)		2.5 µl
10X PCR Reaction Buffer		5.0 µl
5 mM each dNTP(s)		2.5 µl
Taq polymerase (5U/µl)		0.3 µl
Water	to 50 µl	

VIICDR3-Linker-VL Fragment

FDTSEQ1 primer (10pmoles/µl)		2.5 µl
VIICDR3BACK primer (10pmolesµl)		2.5 µl
10X PCR Reaction Buffer		5.0 µl
5 mM each dNTP(s)		2.5 µl
Taq polymerase (5U/µl)		0.3 µl
Water	to 50 µl	

Linker-VL Fragment

FDTSEQ1 primer (10pmoles/µl)		2.5 µl
LINKPCRL primer (10pmolesµl)		2.5 µl
10X PCR Reaction Buffer		5.0 µl
5 mM each dNTP(s)		2.5 µl
Taq polymerase (5U/µl)		0.3 µl
Water	to 50 µl	

Miniprep DNA was prepared from the library described by Marks et al. (1991) as template for PCR. PCR produced from the clone was prepared by innoculating from a bacterial colony.

PCR conditions were 25 cycles of 94° C 1 minute, 55° C 1 minute, 72° C 2 minutes with a final 10 minutes at 72° C.

Primary PCR products were gel purified using the Promega Magic PCR Prep System

except for the CDR3 fragment which requires Mermaid purification (Bio 101) due to its maller size.

CDR1+2 Shuffling

Assembly Of Library CDR1+2 Fragments With The VH CDR3-LinkerVL Fragment From An Isolated Clone

Purified library CDR1+2 DNA	20-50 ng
Purified VHCDR3-Linker-VL Fragment from an isolated clone	20-50 ng
10X PCR Buffer	5.0 µl
5 mM each dNTP(s)	2.5 µl
Taq polymerase (5U/µl)	0.3 µl
Water to 50 µl	

PCR conditions as for primary PCRs.

Secondary PCR Of Assembled CDR1+2 Shuffled DNA

Assembly product	1.0 µl
FDTSEQ1 primer (10pmoles/µl)	2.5 µl
LMB3 primer (10pmoles/µl)	2.5 µl
10X PCR Reaction Buffer	5.0 µl
5 mM each dNTP(s)	2.5 µl
Taq polymerase (5U/µl)	0.3 µl
Water to 50 µl	

CDR3 Shuffling

Assembly Of Library CDR3 Fragments With The CDR1+@ Fragment From An Isolated Clone

Purified library CDR 3 DNA	20-50 ng
Purified CDR1+2 from an isolated clone	20-50 ng
10X PCR Buffer	5.0 µl
5 mM each dNTP(s)	2.5 µl
Taq polymerase (5U/µl)	0.3 µl
Water to 50 µl	

Second PCR Of Assembled Library CDR3 - CDR1+2 From An Isolated Clone

Assembly product	1.0 µl
PCRHLINK primer	

Example 11

Derivation Of Human Catalytic Antibodies By "Imprinting"

The process of "imprinting" involves using an existing antibody with desired binding characteristics, to derive new antibodies, with similar characteristics. This is done by recombining original antibody chains, or parts thereof, with a library of complementary parts. When new antibody elements are found, which complement the original antibody binding characteristics, these are recombined with a library which replaces the original antibody binding characteristics, these are recombined with a library which replaces the original antibody part, to give an entirely new antibody which mimics the binding of the original antibody (PCT/GB/92/01755). This approach might be used to derive human catalytic antibodies from an existing mouse catalytic antibody.

This example describes a "two-step conversion". This, of course, may be done over multiple steps or in a single step, if a hybrid molecule consisting of part of the original antibody is sufficient.

This is a useful method for deriving human antibodies with similar binding activities to an existing mouse antibody for example.

The catalytic phage antibody clones 18 and 83 (see Example 5.2) in pCANTAb vectors, (cloned in pCANTAB vectors), were used as template for PCR amplification of separate heavy and light chains. Heavy chains were amplified with LMB3 and PCRHLINK and light chains were amplified with LINKPCRL and FDTSEQ1 as described above. Libraries of human heavy and light chains were also amplified by PCR using the samer primers and with DNA prepared from the human scFv library described by Marks et al., J. Mol. Biol. 222 (1991):581-597 as described above.

The individual mouse heavy chains from each clone were then recombined with the library of human light chains by PCR linkage as described above. Similarly, the individual light chains were recombined with the library of heavy chains in the same way.

The resulting linked products were cleaved with ApaL1 (for mouse heavy chains) or

SFi1 (for human heavy chains) along with Not1, ligated into the appropriate pCANTAB vector and transformation into *E. coli* TG1 cells. All steps were as described above.

Individual populations of TG1 cells carrying each separate library, were grown for 2-3 hours at 30° C and rescued by infection with VCSM13 helper phage at 37° C. After overnight growth phage particles were collected and concentrated. Each population was panned several times against RT3-BSA and indivdual binding clones identified by ELISA.

Binding clones were selected and the human chain of each clone was amplified by PCR as before. This chain was recombined with the PCR product of the human library of complementary chains. PCR linkage, cleavage with SFi1 and Not1, ligation, transformation, phage rescue, panning and screening were as before.

In this way, a new population of RT3 binders were derived whose binding profile was directed by the original mouse clone but which were entirely human. The above example covers imprinting by shuffling separate chains but could equally apply to shuffling parts of chains in a single or multiple rounds (as above). The library material was derived from the library of Marks et al. J. Mol. Biol. 222 (1991):581-597 but could equally come from PCR products of human blood, spleen, etc., or could be partially or totally derived from synthetic DNA.

The example given above involves shuffling chains within a single chain Fv on a single replicon. A similar result can be achieved by using non-linked VH/VL or VH-CHG/VL-CL fragments displayed on phage (McCafferty et al. WO 92/01047). These again may be on the same replicon or may be on different replicons. For example, the heavy chain of the original mouse antibody may be cloned into pUC19 or other plasmid, in frame with appropriate promoters, signal peptide and stop codon(s) enabling it to be expressed as a soluble VH or VH-CH1 fragment in the bacterial periplasm (Better et al., 1989; Skerra et al., 1989). A growing culture of cells carrying this plasmid could then be infected with helper phage derived from a library of human light chains (either VL or VL-CL, as appropriate), cloned as fusions with gene III in fd-CAT1 or fd-DOG1 (McCafferty et al., supra. 1991) for example. This will give rise to a population of phage expressing indivudal human light chain fused to gene III,

with a heavy chain partner derived from the mouse clone. Those human chains, which complement the binding activity of the mouse chain, will be enriched by panning (McCafferty, et al., supra. 1991) and the gene encoding this chain will be present in the phage particle.

Light chains derived in this way can be recloned into a vector for soluble expression of the single chain in the periplasm, as was done for the original mouse chain. As before, a growing culture of cells expressing these individual human light chains could be infected with helper phage derived from a library of human heavy chains, cloned as fusions with gene III in fd-CAT1 or fd-DOG1 (McCafferty et al., supra. 1991) for example. As before panning against antigen with enrich those clones with the appropriate binding activity. This will result in a pair of human clones which mirror the binding of the original mouse clone.

A similar process can be carried out by shuffling with the human heavy chain first and then the light chain. Alternatively, the enriched population or clones derived from one round of separate shuffling of heavy and light chains can be recombined with each other in the same way as described above for either SCFv(s) or separate chains.

WHAT IS CLAIMED IS

1. A method for producing catalytic antibodies displayed on phage comprising the steps of:

(a) generating a gene library of antibody-derived domains;

(b) inserting coding for said domains into a phage expression vector; and

(c) isolating said catalytic antibodies.

2. A method as recited in Claim 1 wherein said catalytic antibodies are single chain antibodies.

3. A method as recited in Claim 1 wherein the antibodies isolated in step (c) are produced in quantity by culturing *E. coli* cells.

4. Catalytic antibodies prepared by the method of Claim 1.

5. A method as recited in Claim 1 wherein said gene library of antibody-derived domains is generated from one or more of the following groups:

(a) gene fragments obtained from lymphocytes from an immunized animal;

b) gene fragments obtained from lymphocytes from a non-immunized animal;

(c) gene fragments obtained by shuffling of VH and VL chains;

(d) gene fragments obtained by shuffling of CDR regions;

(e) gene fragments obtained by mutagenesis of CDR regions;

(f) imprinting; or

(g) synthetic antibody genes.

6. A method for isolating catalytic antibodies displayed on phage comprising the following steps:

(a) preparing an antigen;

(b) immunizing with said antigen;

(c) generating a library of VH and VL domains from said immunized animal;

(d) cloning said VH and VL domains into a phage expression vector to generate

phage display antibodies;

(e) selecting phage display antibodies which bind specifically to said antigen;

(f) screening said selected phage display antibodies for catalytic activity to substrate; and

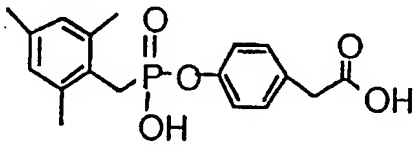
(g) isolating said catalytic antibodies.

7. A method as recited in Claim 6 wherein said cataltyic antibodies are single chain antibodies.

8. A method as recited in Claim 6 wherein said antigen is a transition state analog.

9. A method as recited in Claim 6 wherein said antigen is a phosphonate.

10. A method as recited on Claim 6 wherein said antigen is



11. Catalytic antibodies prepared by the method of Claim 6.

12. A method for isolating catalytic human antibodies displayed on phage comprising the following steps:

(a) preparing an antigen;

(b) generating a library of VH and VL domains;

(c) cloning said VH and VL domains into a phage expression vector to generate phage display antibodies;

(d) selecting phage display antibodies which bind specifically to said antigen;

(e) screening said selected phage display antibodies for catalytic activity to substrate; and

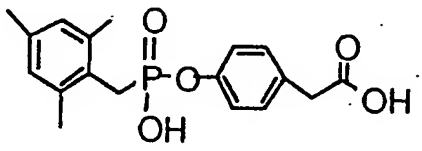
(f) isolating said catalytic antibodies.

13. A method as recited in Claim 12 wherein said library is mouse-derived.

14. A method as recited in Claim 12 wherein said antigen is a transition state analog.

15. A method as recited in Claim 12 wherein said antigen is a phosphonate.

16. A method as recited in Claim 12 wherein said antigen is



17. Catalytic antibodies prepared by the method of Claim 12.

18. A method for producing catalytic antibodies displayed on phage through chain shuffling comprising the following steps:

(a) combining a library of VL genes with VH genes to form a chain shuffled library;

(b) cloning the shuffled chain;

(c) expressing said chain shuffled antibody on phage;

(d) selecting against an antigen; and

(e) screening for catalytic activity.

19. A method for producing catalytic antibodies displayed on phage through CDR shuffling comprising the following steps:

(a) isolating VL and VH genes;

(b) isolating a library of CDR regions;

(c) recombining said VL and VH genes with said library of CDR regions to produce a CDR shuffled library; and

(d) cloning the CDR shuffled library;

(e) expressing said CDR shuffled library on phage;

(f) selecting against an antigen; and

(g) screening for catalytic activity.

20. A method for producing catalytic antibodies displayed on phage through imprinting

comprising the following steps:

(a) selecting a set of antibodies;

(b) isolating a set of VH and a set of VL genes from said antibodies;

(c) combining said set of VH with a library of VL and combining said set of VL with a library of VH to form two combination libraries;

(d) cloning said combination libraries;

(e) expressing said libraries on phage;

(f) selecting against an antigen;

(g) isolating selected libraries of VH and VL genes;

(h) combining said libraries of VH and VL genes;

(i) cloning said combined libraries;

(j) expressing said combined libraries on phage;

(k) reselecting against an antigen; and

(l) screening for catalytic activity.

21. A recombinant cloning vector comprising an antibody, 6 His residues, a portion of a myc gene, and a phage gene III.

22. A recombinant cloning vector of Claim 21 wherein said vector allows the production of a fusion protein consisting of the following elements: an antibody which retains binding activity, a His-6 sequence which retains metal ion binding activity, and a myc sequence which retains antigenicity.

23. A recombinant cloning vector of Claim 21 wherein said vector allows production of a fusion protein consisting of the following elements: an antibody which retains binding activity, a His-6 sequence, a myc sequence, and a gene III protein which retains biological activity.

24. A method for enhancing the rate of cleavage or formation of a specific bond within a molecule *in vivo* which comprises introducing into an animal an effective amount of a phage-derived catalytic antibody.

25. A method for *in vivo* activation of a prodrug comprising:

(a) introducing a prodrug into a patient, said prodrug having a chemical bond

therein which upon cleavage releases the active form of said drug; and

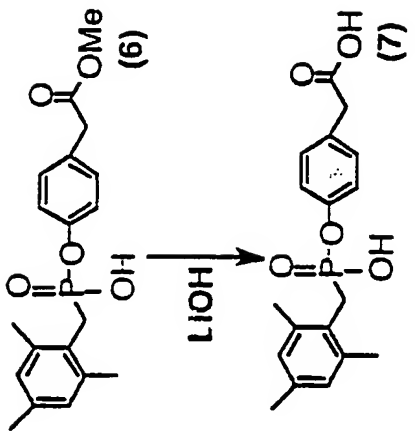
(b) introducing into said patient an effective amount of a phage-derived catalytic antibody capable of cleaving said bond in said prodrug.

26. A method for activating or deactivating a biological function in an animal by enhancing the rate of cleavage or formation of a specific bond within a molecule *in vivo* which comprises introducing into an animal an effective amount of a catalytic antibody, said antibody having been produced by the method of Claim 1.

27. A method for activating or deactivating a biological function in an animal by enhancing the rate of cleavage or formation of a specific bond within a molecule *in vivo* which comprises introducing into an animal an effective amount of a catalytic antibody, said antibody having been produced by the method of Claim 18.

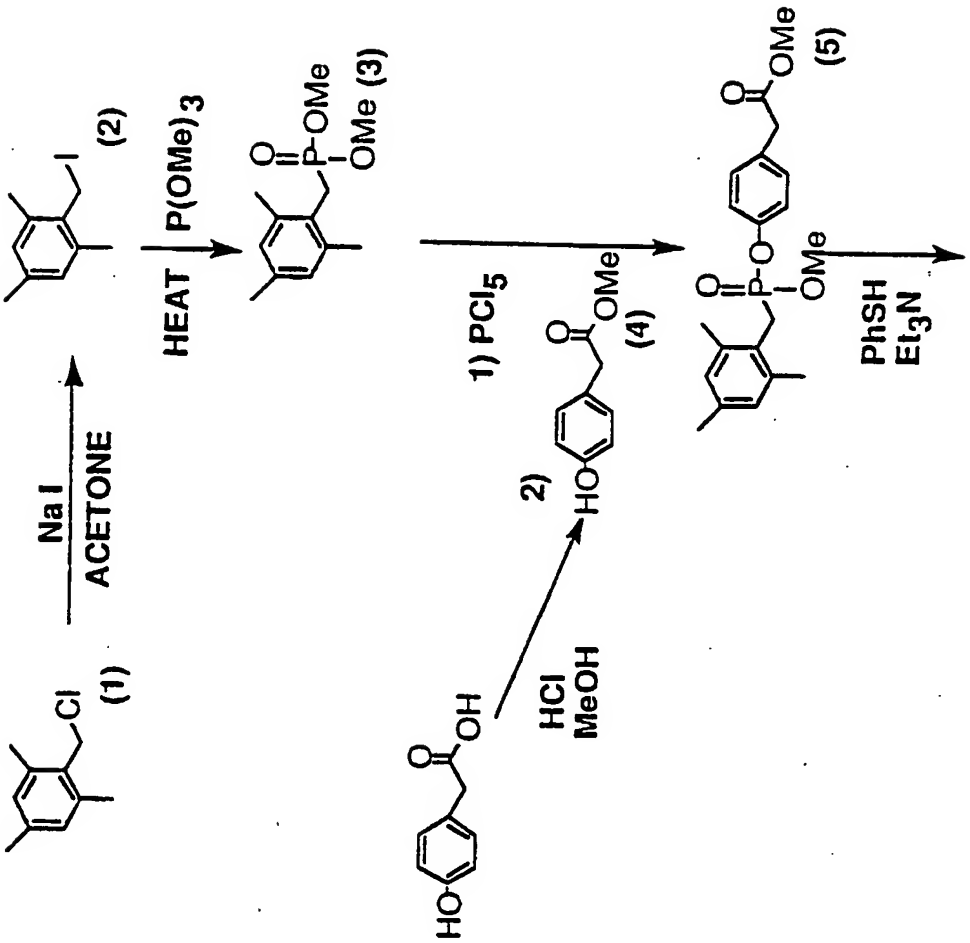
28. A method for activating or deactivating a biological function in an animal by enhancing the rate of cleavage or formation of a specific bond within a molecule *in vivo* which comprises introducing into an animal an effective amount of a catalytic antibody, said antibody having been produced by the method of Claim 19.

29. A method for activating or deactivating a biological function in an animal by enhancing the rate of cleavage or formation of a specific bond within a molecule *in vivo* which comprises introducing into an animal an effective amount of a catalytic antibody, said antibody having been produced by the method of Claim 20.



RT3 Phosphonate TSA

Figure 1


Cl
(1)
Na I
ACETONE
I
(2)
HEAT
P(OMe)3
O
P
OMe
OMe (3)
1) PCl5
2)
HO
OH
O
HCl
MeOH
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(4)
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OMe
OMe
(5)
PhSH
Et3N

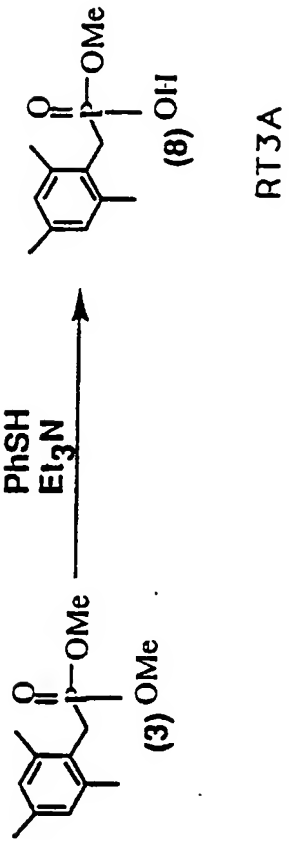


Figure 2

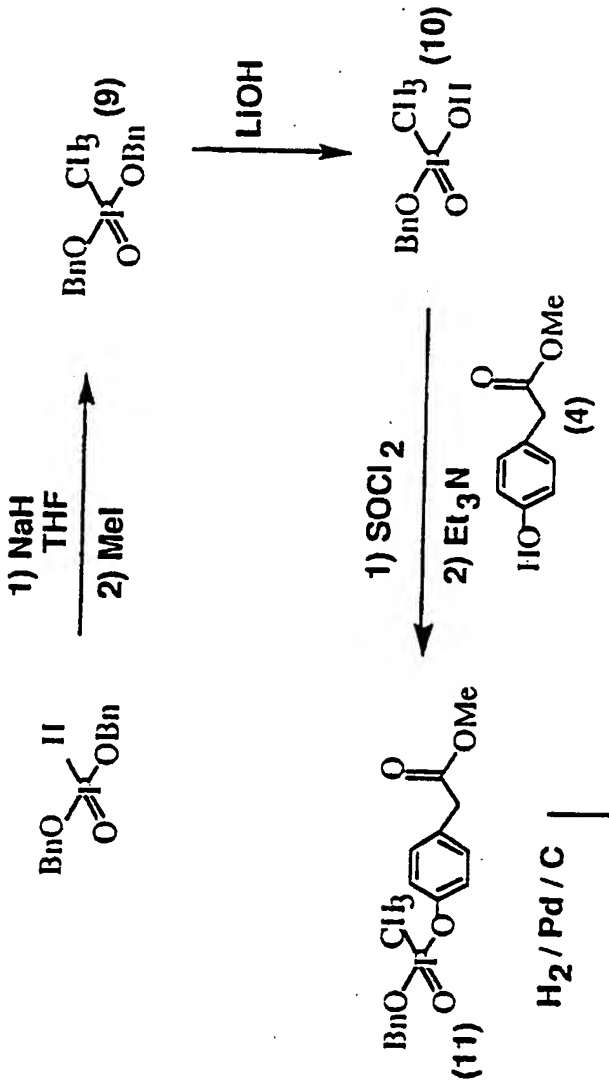


Figure 3

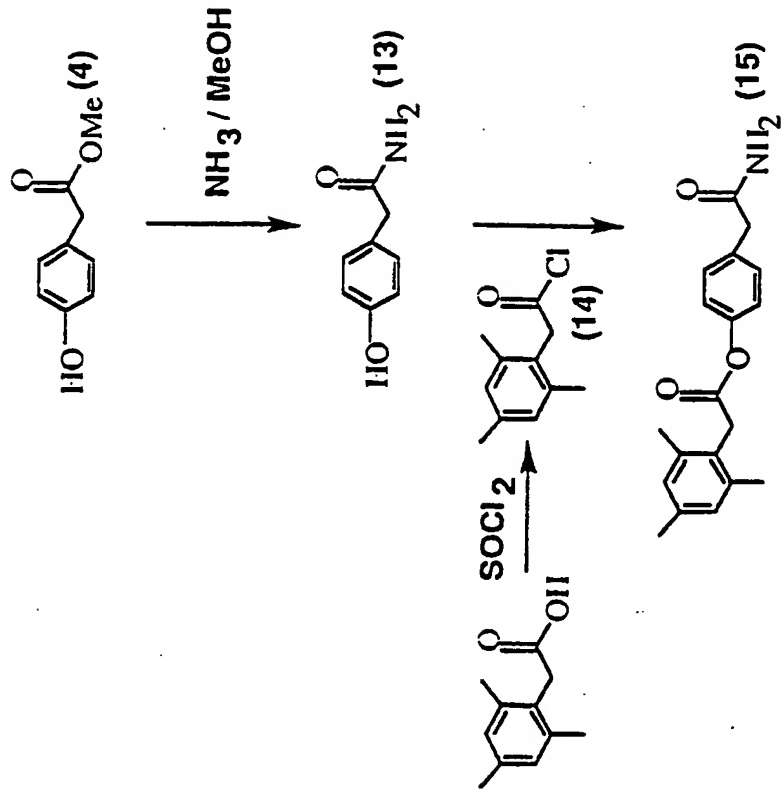


Figure 4

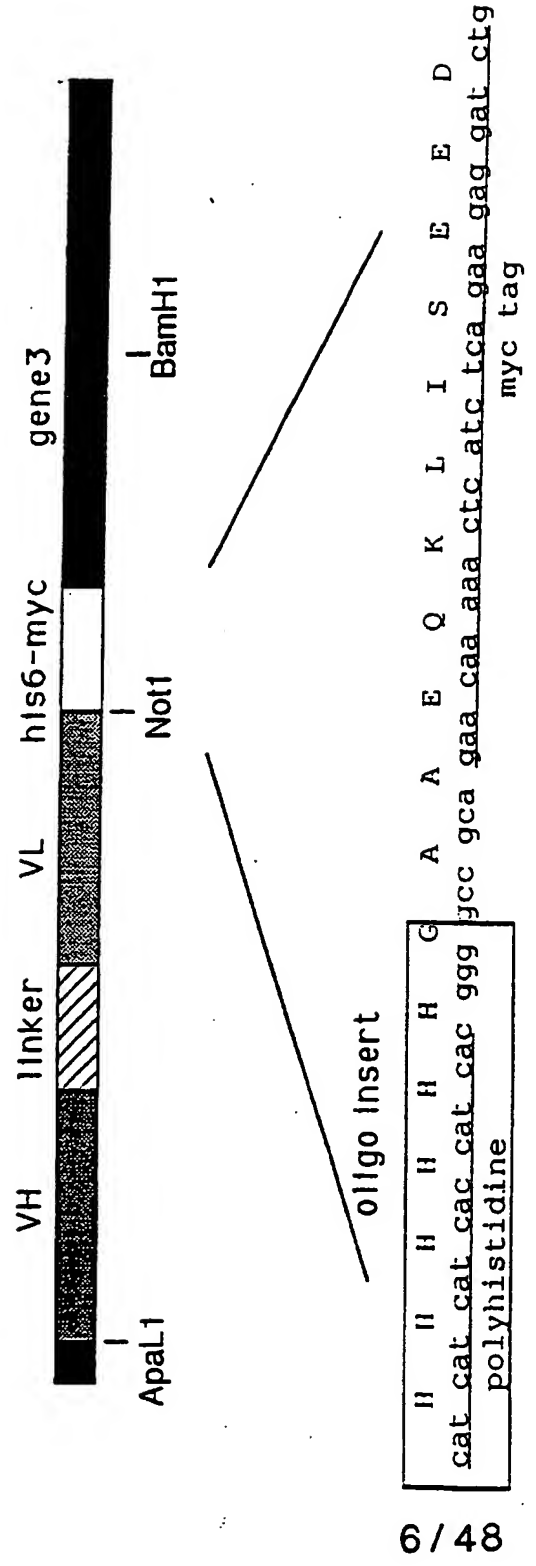

VH
linker
VL
his6-myc
gene3
ApaL1
Not1
BamH1
oligo insert
H H H H H G A A E Q K L I S E E D
cat cat cac cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag gat ctg
polyhistidine
myc tag

Figure 5

L N G A A amber '
aat ggg gcc gca tag-gene3 3'

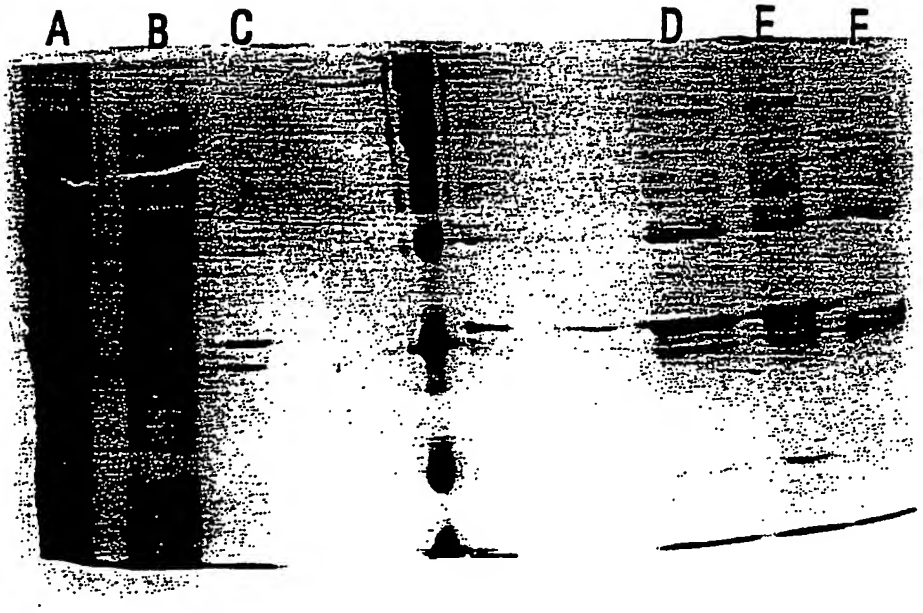


Figure 6

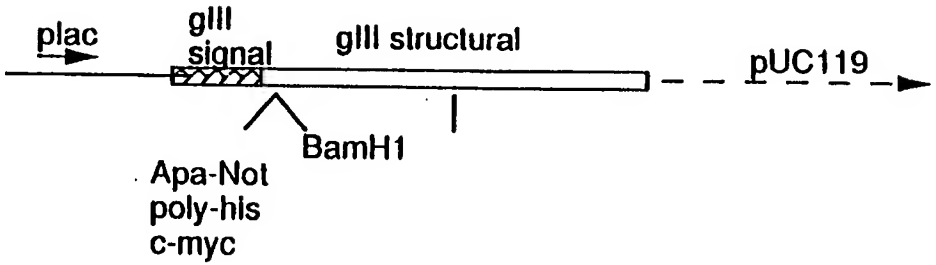
gIII/pelB LEADER

V K K L L F A I P L V V P F Y A A Q P A
GTG AAA AAA TTA TTA TTC GCA ATT CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC

SfiI NcoI Pst1 Xho I Not I

H H H H H H G A A E Q K L I S E E D L N G A A Amber
cat cat cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag gat ctg aat ggg gcc gca tag-gene3
polyhislidine myc tag

Figure 7



pCANTAB-3his6

LEADER -1 +1 POLYLINKER

H S A Q V Q L Q E L E I K R A A A

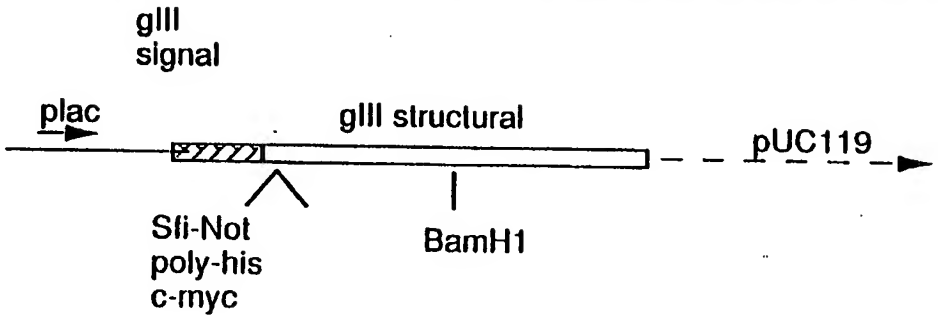
CAC AGT GCA CAG GTC CAA CTG CAG GAG CTC GAG ATC AAA CGG GCG GCC GCA

Apa LI Pst I Xho I N

H H H H H H G A A E Q K L I S E E D L N G A A Amber

cat cat cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag gat ctg aat ggg gcc gca tag-gene3

polyhistidine myc tag



pCANTAB-5his6

-1 POLYLINKER

M A I Q V Q L E L I K R A A A

ATG GCC CAG GTC CAA CTG CAG GAG CTC GAG ATC AAA CGG GCG GCC GCA

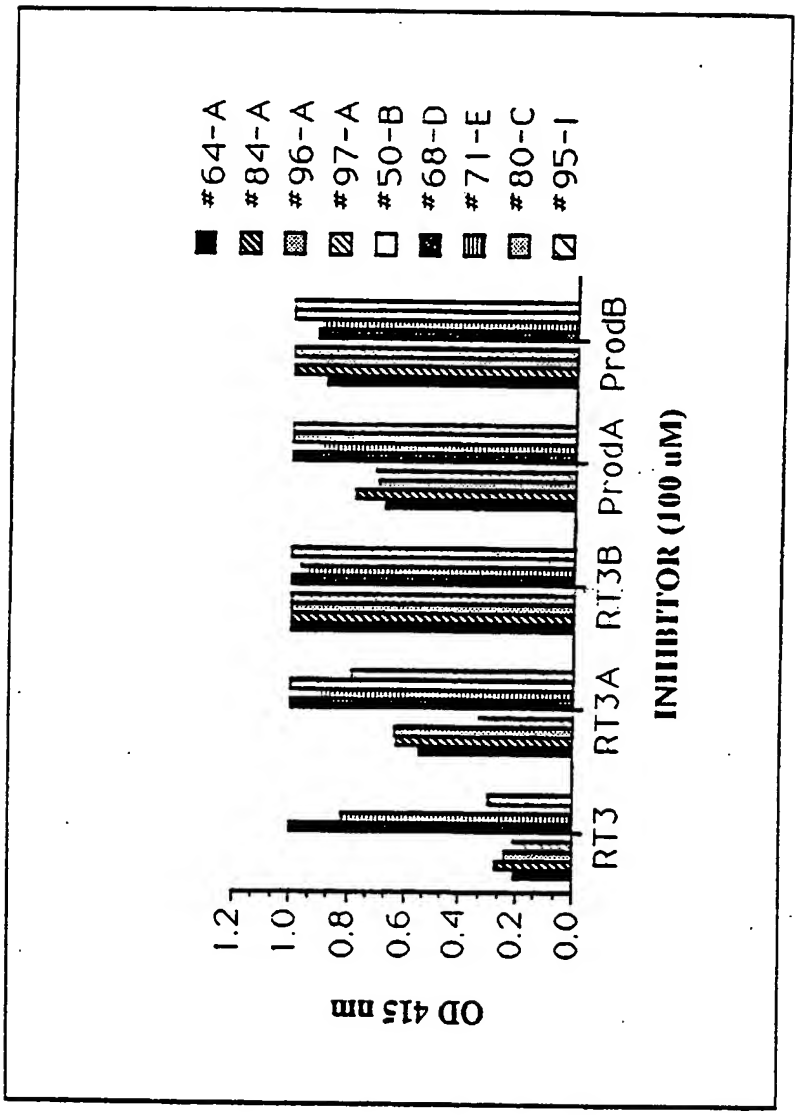
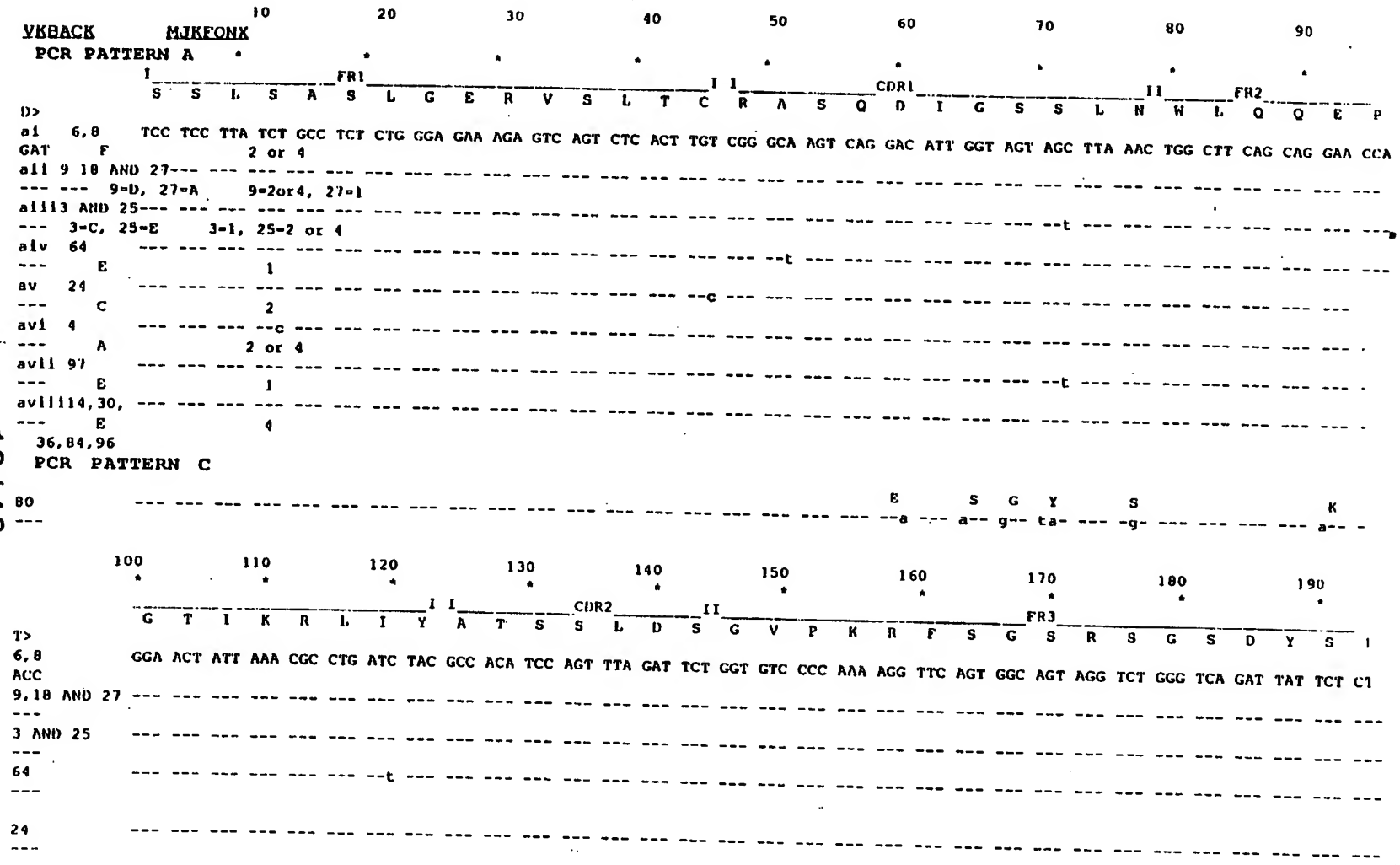

#64-A
#84-A
#96-A
#97-A
#50-B
#68-D
#71-E
#80-C
#95-I
OD 415 nm
0.0
0.2
0.4
0.6
0.8
1.0
1.2
RT3
RT3A
RT3B
ProdA
ProdB
INHIBITOR (100 uM)

Figure 8



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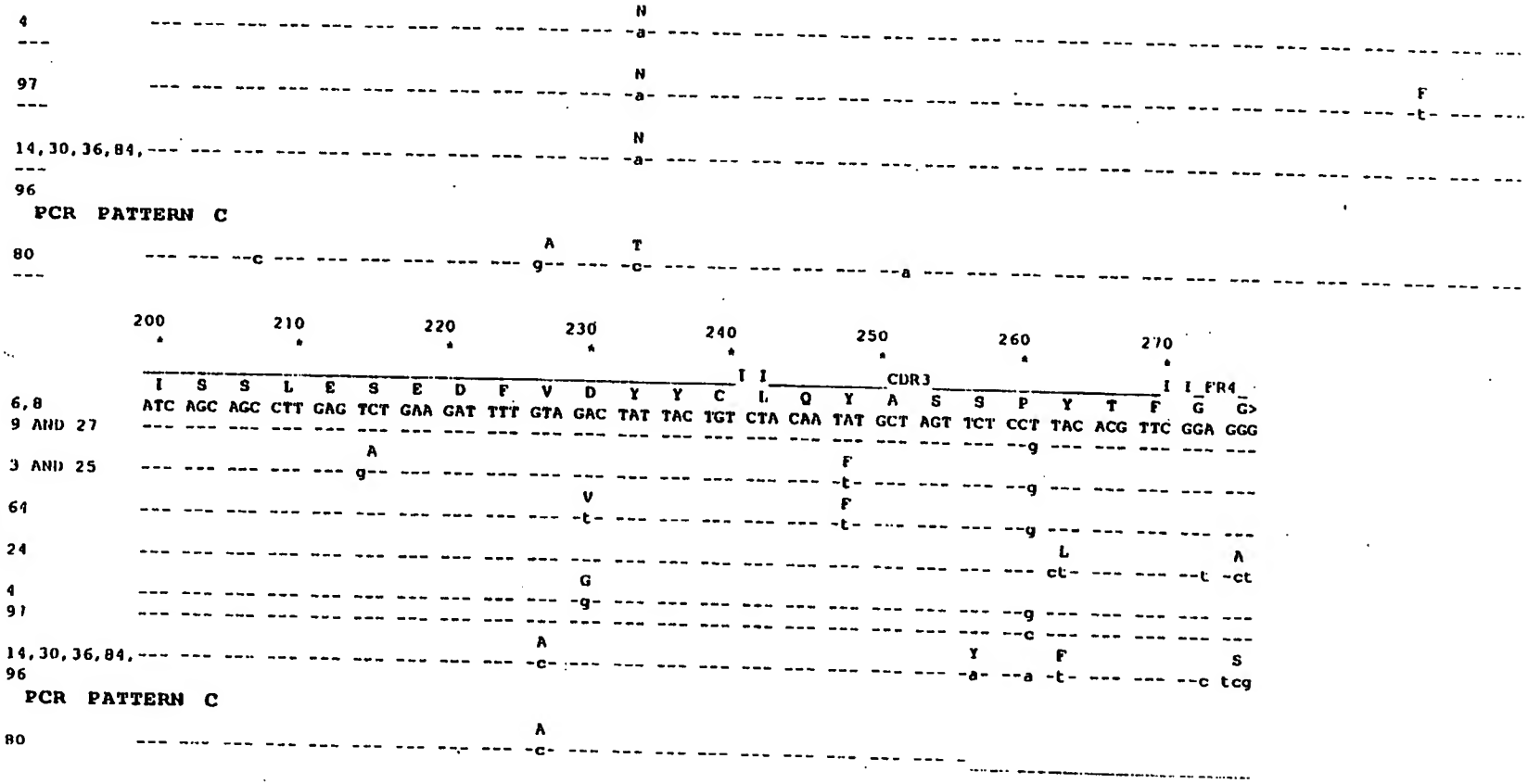
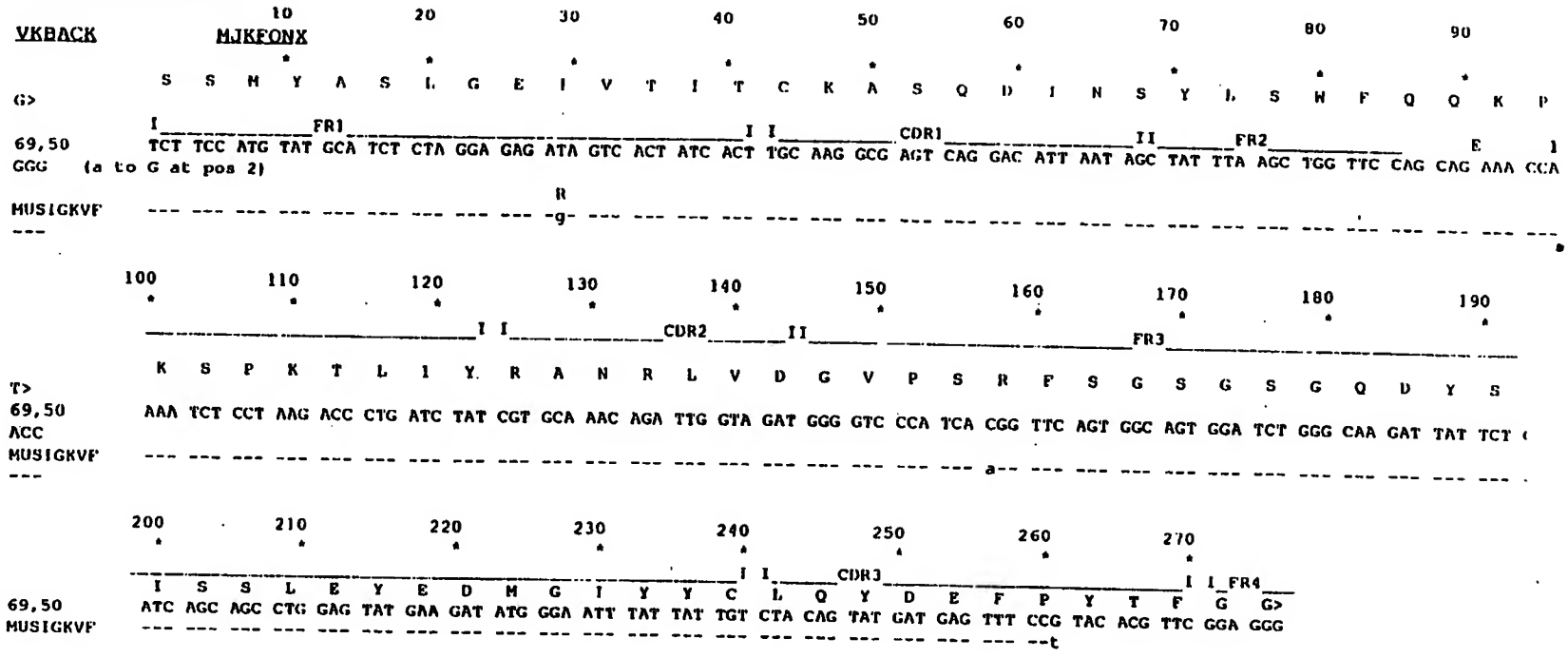
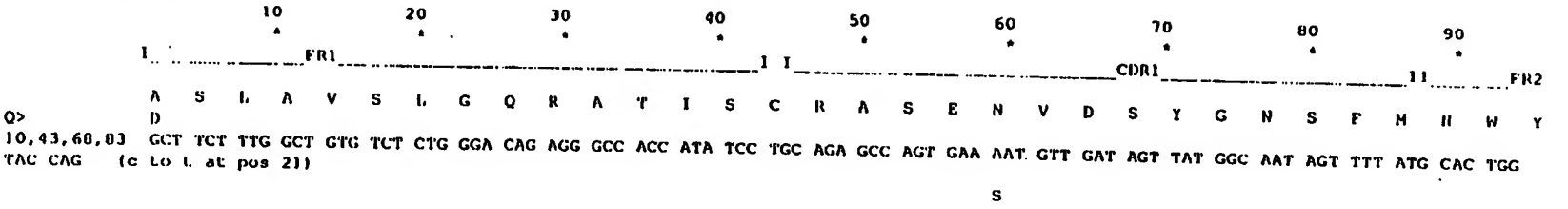

4
97
14,30,36,84,96
PCR PATTERN C
80
PCR PATTERN C
80
200
210
220
230
240
250
260
270
CDR3
FR4
6,8 AND 27
3 AND 25
64
24
4
97
14,30,36,84,96

Figure 9

PCR PATTERN B



PCR PATTERN D



```
MUSIGKVR2  --- --- --- --- --- --- --a --g --- --- --- --- --- --- --- --- --- --- --- -g- --- --- --- --- --- --- --- --- --- --- --- ---
germline
           100        110        120        130        140        150        160        170        180        190
            *          *          *          *          *          *          *          *          *          *
                                                    I I______CDR2_________II_________FR3____________________________
            Q   K   S   G   Q   P   P   K   L   L   I   Y   L   A   S   N   L   Q   S   G   V   P   A   R   F   S   G   S   G   S   R   T
D>
10,43,68,83 CAG AAA TCA GGA CAG CCA CCC AAA CTC CTC ATC TAT CTT GCA TCC AAC CTA CAA TCT GGG GTC CCT GCC AGG TTC AGT GGC AGC GGG TCT AGG
ACA GAC
                P                                                E
MUSIGKVR2  --- --- c-- --- --- --- --- --- --- --- --- --- --- --- --- --- --- g-- --- --- --- --- --- --- --- --- -t --- --- --- ---
---
germline
           200        210        220        230        240        250        260        270
            *          *          *          *          *          *          *          *
                                                                        I I_____CDR3___________________I 1_FR4___
            F   T   L   T   I   D   P   V   E   A   D   D   A   A   T   Y   Y   C   L   Q   N   T   E   D   P>
10,43,68   TTC ACC CTC ACC ATT GAT CCT GTG GAG GCT GAT GAT GCT GCA ACC TAT TAC TGT CTG CAA AAT ACT GAG GAT CCG
                                                                            Q       N
MUSIGKVR2  --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -a- --- --- -a- --- --- --t
```

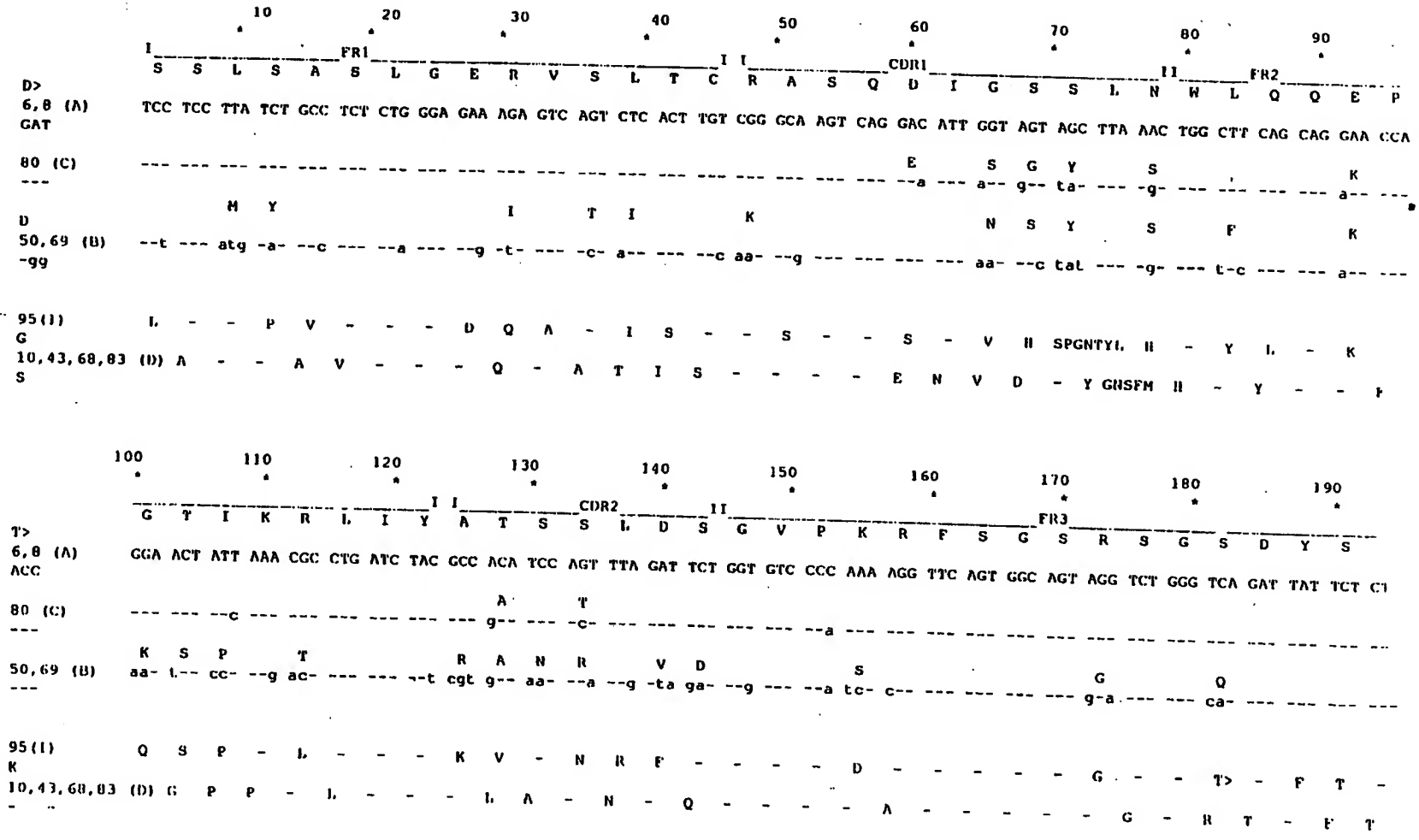
PCR PATTERN I

VKBACK MJKFONX

```
           10         20         30         40         50         60         70         80         90
            *          *          *          *          *          *          *          *          *
      I_________FR1_____________________________I I_________________CDR1______________________________II___FR2
            L   S   L   P   V   S   L   G   D   Q   A   S   I   S   C   R   S   S   Q   S   L   V   H   S   P   G   N   T   Y   L   H
Y>
95         CTC TCC CTG CCT GTC AGT CTT GGA GAT CAA GCC TCC ATC TCT TGC AGA TCT AGT CAG AGC CTT GTA CAC AGT CCT GGA AAC ACC TAT TTA CAT T
TAC
                                                                                            N
MUSIGKVD   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- aa- --- --- --- --- --- --- -
---
           100        110        120        130        140        150        160        170        180        190
            *          *          *          *          *          *          *          *          *          *
                                                    I I_____CDR2__________II_________FR3_____________________________
            L   Q   K   P   G   Q   S   P   K   L   L   I   Y   K   V   S   N   R   F   S   G   V   P   D   R   F   S   G   S   G   S   G
T>
95         CTG CAG AAG CCA GGC CAG TCT CCA AAG CTC CTG ATC TAC AAA GTT TCC AAC CGA TTT TCT GGG GTC CCA GAC AGG TTC AGT GGC AGT GGA TCA GGG
ACA
MUSIGKVD   --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
---
           200        210        220        230        240        250        260        270
```

95
MUSIGKVII
D F T L K I S R V E A E D L G V Y F C S Q S T H V P
GAT TTC ACA CTC AAG ATC AGC AGA GTG GAG GCT GAG GAT CTG GGA GTT TAT TTC TGC TCT CAA AGT ACA CAT GTT CCG
10 20 30 40 50 60 70 80 90
CDR3
FR4

Figure 10


10 20 30 40 50 60 70 80 90
FR1 CDR1 FR2
S S L S A S L G E R V S L T C R A S Q D I G S S L N W L Q Q E P
D>
6,8 (A) TCC TCC TTA TCT GCC TCT CTG GGA GAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC ATT GGT AGT AGC TTA AAC TGG CTT CAG CAG GAA CCA GAT
80 (C) --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --a --- a-- g-- ta- --- -g- --- --- --- --- a-- --- ---
D M Y I T I K N S Y S F K
50,69 (B) --t --- atg -a- --c --- --a --- --g -t- --- -c- a-- --- --c aa- --g --- --- --- --- aa- --c tat --- -g- --- t-c --- --- a-- --- -gg
95(I) L - - P V - - - D Q A - I S - - S - - S - V H SPGNTYL H - Y L - K G
10,43,68,83 (D) A - - A V - - - Q - A T I S - - - - - E N V D - Y GHSFM H - Y - - F S
100 110 120 130 140 150 160 170 180 190
CDR2 FR3
G T I K R L I Y A T S S L D S G V P K R F S G S R S G S D Y S
T>
6,8 (A) GGA ACT ATT AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GAT TCT GGT GTC CCC AAA AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CT ACC
80 (C) --- --- --c --- --- --- --- --- --- A g-- --- T -c- --- --- --- --- --- --a --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
K S P T R A N R V D S G Q
50,69 (B) aa- t-- cc- --g ac- --- --- --t cgt g-- aa- --a --g -ta ga- --g --- --a tc- c-- --- --- --- --- g-a --- --- ca- --- --- --- --- ---
95(I) Q S P - L - - - K V - N R F - - - - D - - - - - G - - T> - F T - K
10,43,68,83 (D) G P P - L - - - L A - N - Q - - - - A - - - - - G - R T - F T - - -

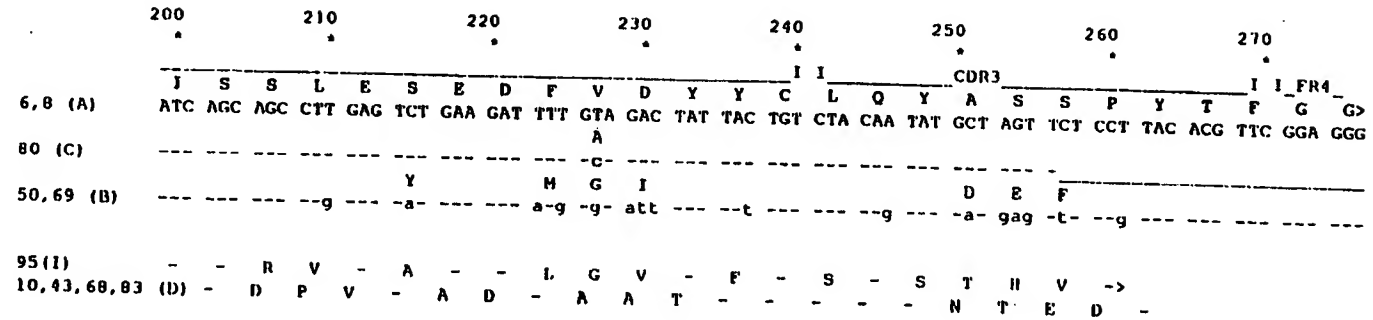
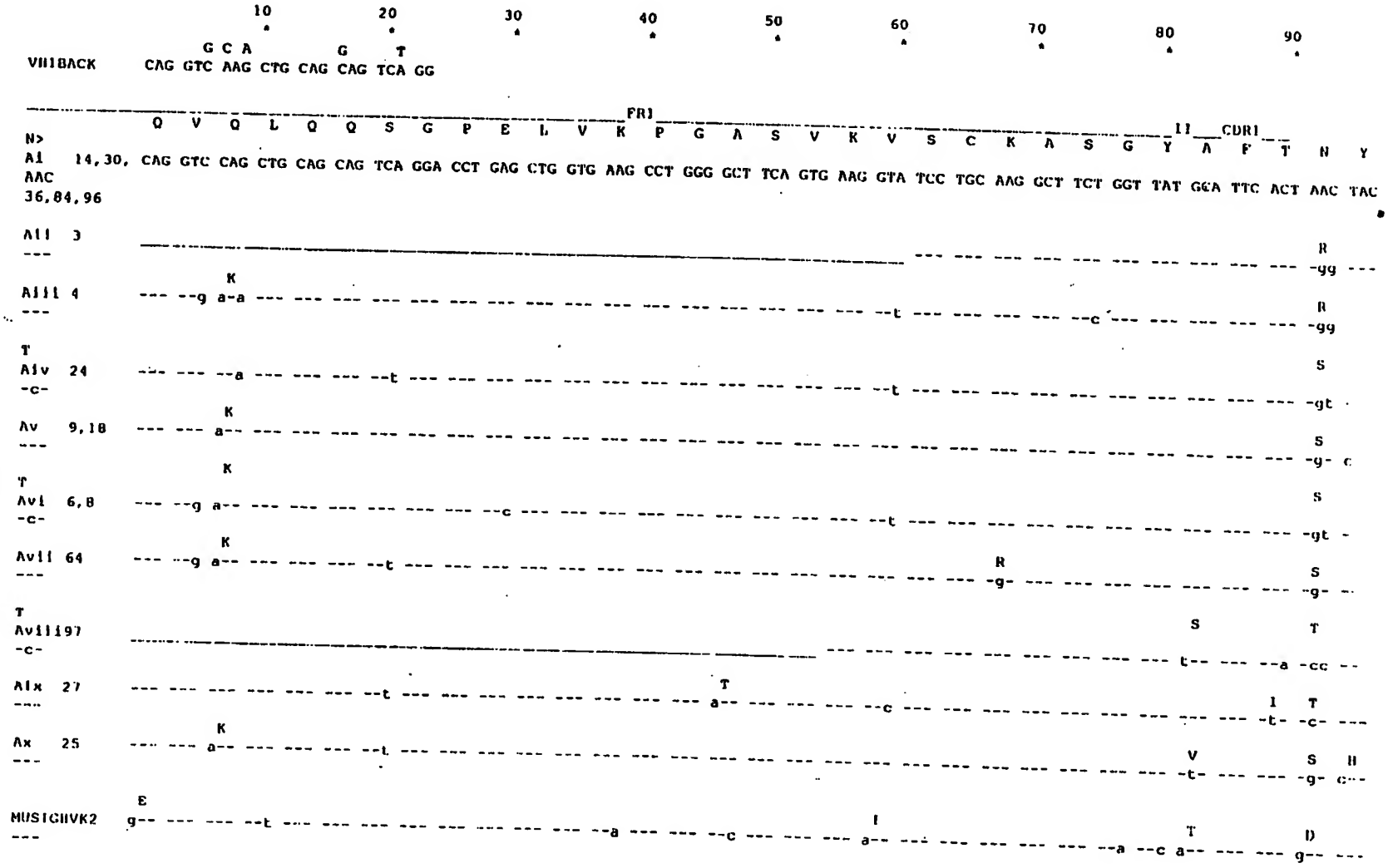

200
210
220
230
240
250
260
270
CDR3
FR4
6,8 (A)
80 (C)
50,69 (B)
95(I)
10,43,68,83 (D)

Figure 11


10 20 30 40 50 60 70 80 90
VHIBACK G C A G T CAG GTC AAG CTG CAG CAG TCA GG
FR1 II CDR1
N> Q V Q L Q Q S G P E L V K P G A S V K V S C K A S G Y A F T N Y
AI 14,30, CAG GTC CAG CTG CAG CAG TCA GGA CCT GAG CTG GTG AAG CCT GGG GCT TCA GTG AAG GTA TCC TGC AAG GCT TCT GGT TAT GCA TTC ACT AAC TAC
AAC 36,84,96
AII 3 R
AIII 4 K R
AIV 24 S
AV 9,18 K S
AVI 6,8 K S
AVII 64 K R S
AVIII197 S T
AIX 27 T I T
AX 25 K V S H
MUSIGHVK2 E I T D

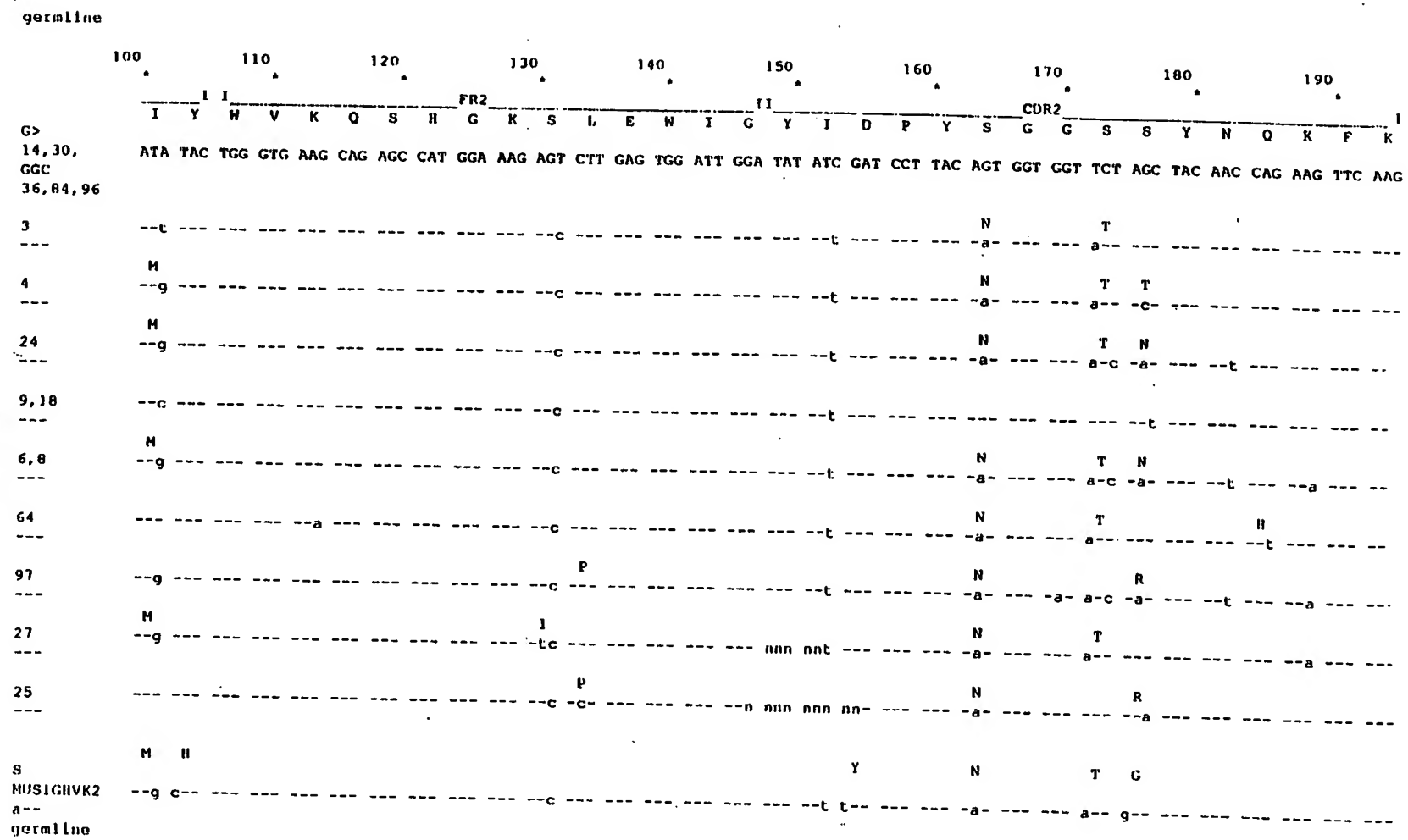
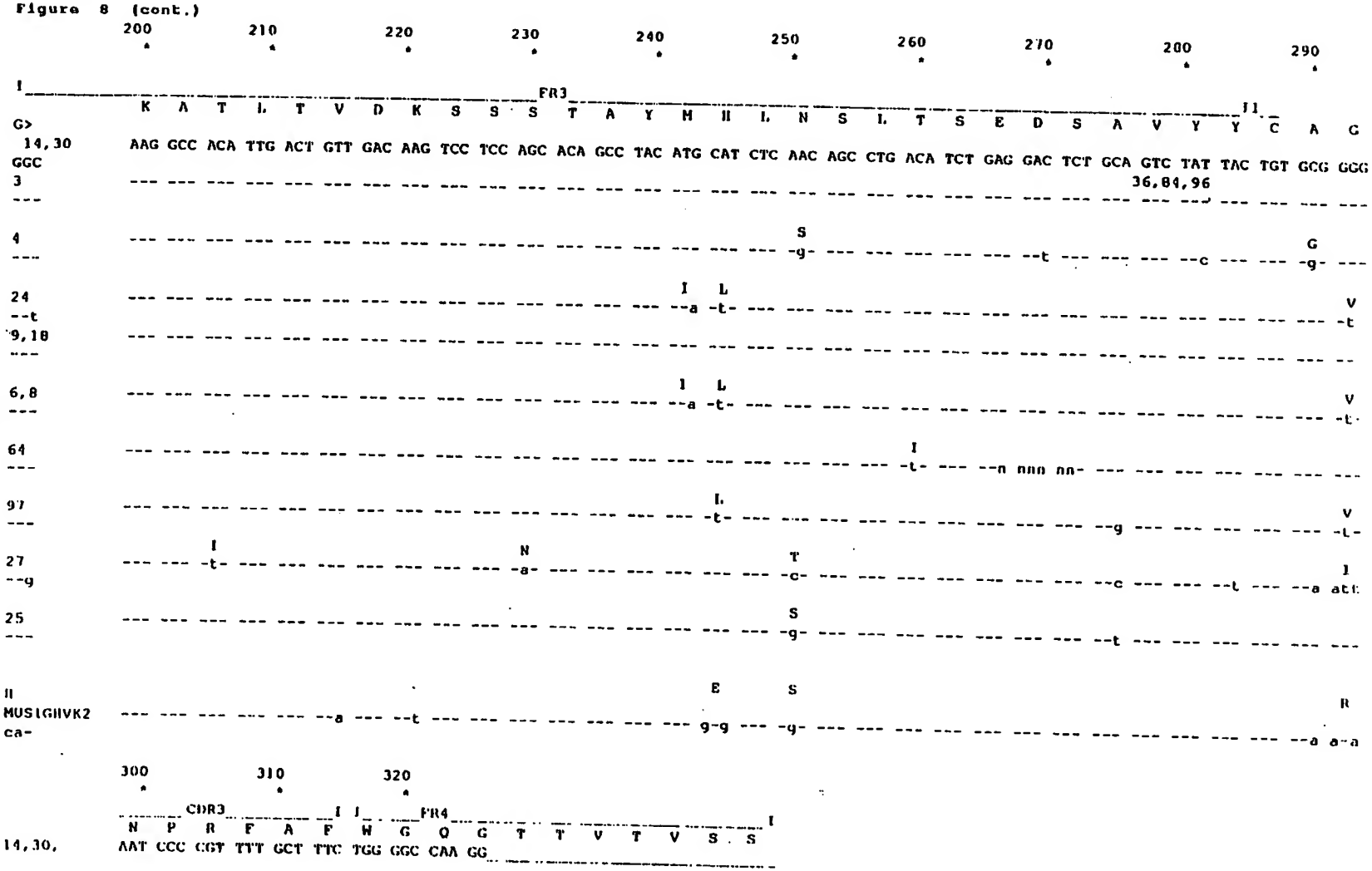

germline
100 110 120 130 140 150 160 170 180 190
I I FR2 II CDR2 I
I Y W V K Q S H G K S L E W I G Y I D P Y S G G S S Y N Q K F K
G>
14,30, GGC 36,84,96
ATA TAC TGG GTG AAG CAG AGC CAT GGA AAG AGT CTT GAG TGG ATT GGA TAT ATC GAT CCT TAC AGT GGT GGT TCT AGC TAC AAC CAG AAG TTC AAG
3
4
24
9,18
6,8
64
97
27
25
S
MUSIGHVK2a--
germline

Figure 8 (cont.)



```
36,84,96
1       --- --- --- --- --- --- --- --- ---
                            G
4       --- --- --- --- -g- --- --- --- ---
                        S       Y
24      --- --- --- --- -c- --- -a- --- ---
                                G
9,18    --- --- --- --- --- -g- --- --- ---
                        S       Y
6,8     --- --- --- --- -c- --- -a- --- ---
                                G
64      --- --- --- --- --- -g- --- --- ---
                        S
97      --- --- --- --- -c- --- --- --- ---
                    Y   D   R   G   Y
27      --- ta- gac aga -g- -a- --- --- ---
25      --- --- --- --- --- --- --- --- ---
                    S
MUS1GIIVK2  ag-

VHFOR-2 (REV)                                   GG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA
```

Figure 12

PCR PATTERN B

```
                          10          20          30          40          50          60          70          80          90
                          .           .           .           .           .           .           .           .           .
I___CDR1___ ___________________________________________________________FR1_______________________________________________I
               X   X   X   X   Q   Q   S   G   P   E   L   V   K   P   G   A   S   V   K   M   S   C   K   A   S   G   Y   T   F . T   S   Y
V>
49,50,69,90 ____________ CAG CAG TCT GGT CCT GAG CTG GTA AAG CCT GGG GCT TCA GTG AAG ATG TCC TGC AAG GCT TCT GGA TAC ACA TTC ACA AGT TAT
GTT
MUSIGHVJ2   ____________ --- --a --- --a --- --- --- --g --- --- --- --- --- --- --- --a --- --- --- --- --- --c --t --c --- --- --c --c
ta-
         100        110        120        130        140        150        160        170        180        190
          .          .          .          .          .          .          .          .          .          .
            ______I I_______________FR2____________________I
I__________ ______________CDR2______________________________I
            H   H   W   V   K   Q   K   P   G   Q   G   L   E   W   I   G   D   I   N   P   Y   N   D   G   T   K   Y   N   E   K   F   I
G>
49,50,69,90 ATG CAC TGG GTG AAG CAG AAG CCT GGG CAG GGC CTT GAG TGG ATT GGA GAT ATT AAT CCT TAC AAT GAT GGT ACT AAG TAC AAT GAG AAG TTC A/
GGC
MUSIGHVJ2   --a --- --- --- --- --- -g- --- --a --- --- --- --- --- --- --- t-- --- t-- --- aga g-- -g- a-- --- --t --- --- --- --- --- --
---
         200        210        220        230        240        250        260        270        280        290
          .          .          .          .          .          .          .          .          .          .
          I______________________________________FR3_____________________________________________________________
I__
            K   A   T   L   T   S   D   K   S   S   N   T   A   Y   M   E   L   S   S   L   T   S   E   D   S   A   V   Y   Y   C   A   G
F>
49,50,69,90 AAG GCC ACA CTG ACT TCA GAC AAA TCC TCC AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG ACC TCT GAG GAC TCT GCG GTC TA? TAC TGT GCG GG
TTT
MUSIGHVJ2   --- --- --- --- --- g-- --- -c- --- --- -g- --- --- --- --- c-- --- --- --- --- --- --a --- --- --- --- --a --- --- -t- --- --a a-
----

            _CDR3_I I_______________FR4___________________I
            A   H   W   G   Q   G   T   T   V   T   V   S   S
49,50,69,90 GCT CAC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA
```

PCR PATTERN D

```
                          10          20          30          40          50          60          70          80          90
                          .           .           .           .           .           .           .           .           .
I___CDR1___ ___________________________________________________________FR1_______________________________________________I
```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```
                Q  V  Q  L  Q  Q  S  G  A  E  L  A  K  P  G  A  S  V  K  M  S  C  K  A  S  G  Y  T  F  T  S  Y
W>
10,26,43,68,83 CAG GTG CAG CTG CAG CAG TCT GGG GCT GAA CTG GCA AAA CCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACC TTT ACT AGC
TAC TGG
MUSIGVH6    --- --c --- --- --- --- --- -ca --- --- --- --- -g- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
ac-

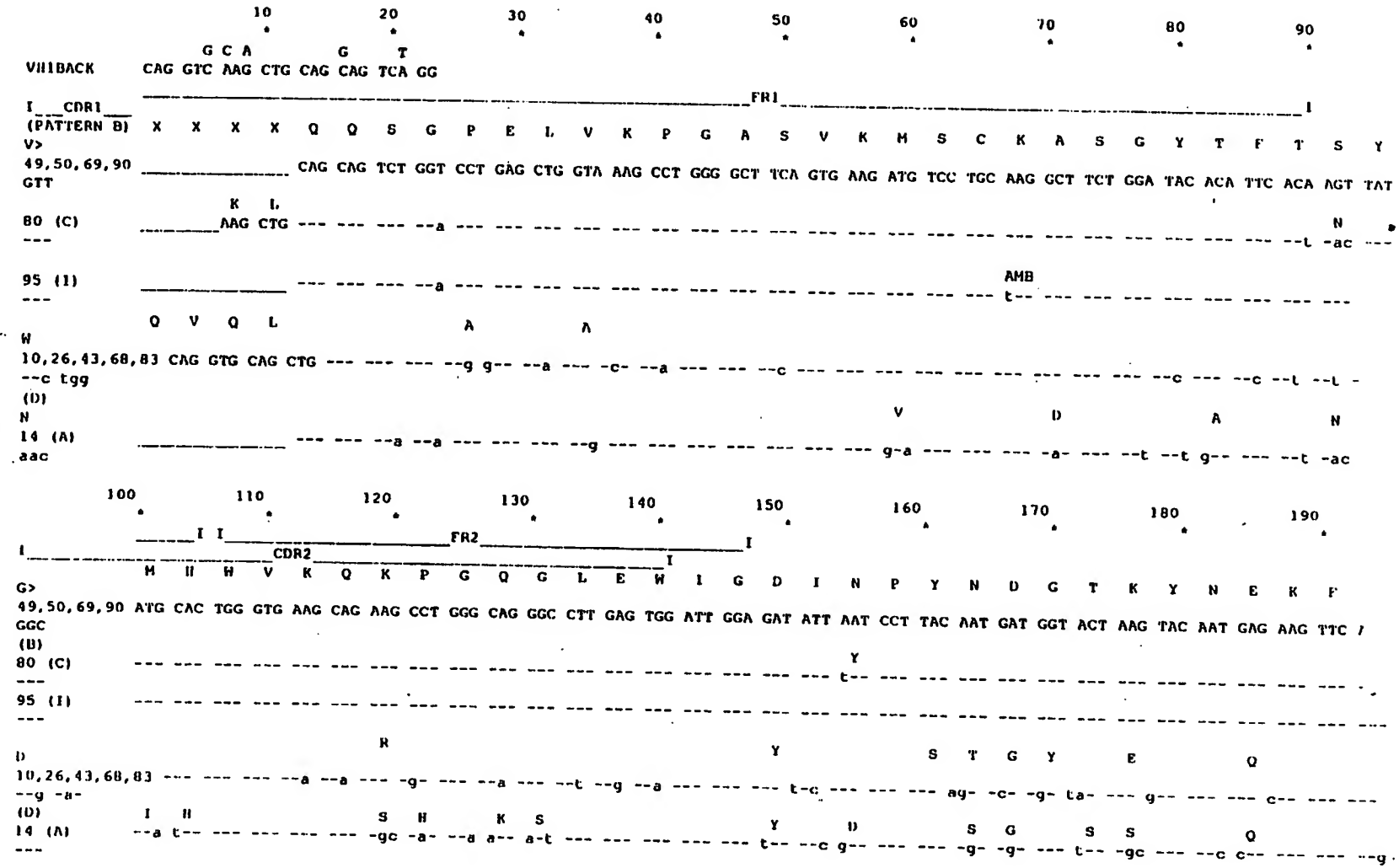
          100         110         120         130         140         150         160         170         180         190
           *           *           *           *           *           *           *           *           *           *
           _____I I_____________________FR2_____________________________I
I__________________CDR2_____________________________I
                H  H  W  V  K  Q  R  P  G  Q  G  L  E  W  I  G  Y  I  N  P  S  T  G  Y  T  E  Y  N  Q  K  F  K
D>
10,26,43,68,83 ATG CAC TGG GTA AAA CAG AGG CCT GGA CAG GGT CTG GAA TGG ATT GGA TAC ATT AAT CCT AGC ACT GGT TAT ACT GAG TAC AAT CAG AAG TTC
AAG GAC
MUSIGVH6    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -g- --a --- --- --- --- --- --- --- --
---

          200         210         220         230         240         250         260         270         280         290
           *           *           *           *           *           *           *           *           *           *
           I_____________________________________________FR3_____________________________________________________________
I__
                K  A  T  L  T  A  D  K  S  S  S  T  A  Y  M  Q  L  S  S  L  T  S  E  D  S  A  V  Y  Y  C  A  R
T>
10,26,43,68,83 AAG GCC ACA TTG ACT GCA GAC AAA TCC TCC AGC ACA GCC TAC ATG CAA CTG AGC AGC CTG ACA TCT GAG GAC TCT GCA GTC TAT TAC TGT GCA
AGA ACG
MUSIGVH6    --- a-- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --g --- --- --- --- --- --
cac

          300         310         320         330
           *           *           *           *
          _____CDR3_____________________I I_____FR4 _____________________________I
                L  Y  Y  Y  A  M  D  Y  W  G  Q  G  T  T
10,26,43,68 TTA TAT TAC TAT GCT ATG GAC TAC TGG GGC CAA GGG ACC ACC GTC ACC GTC TCC TCA
MUSIGVH6    agt gg- gca

VHFOR-2(REV)                                GG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA
```

Figure 13


10 20 30 40 50 60 70 80 90
G C A G T
VH1BACK CAG GTC AAG CTG CAG CAG TCA GG
I__CDR1__ FR1 I
(PATTERN B) X X X X Q Q S G P E L V K P G A S V K M S C K A S G Y T F T S Y
V>
49,50,69,90 CAG CAG TCT GGT CCT GAG CTG GTA AAG CCT GGG GCT TCA GTG AAG ATG TCC TGC AAG GCT TCT GGA TAC ACA TTC ACA AGT TAT
GTT
K L
80 (C) AAG CTG --- --- --- --a --- --t -ac ---
---
95 (I) --- --- --- --a ---

Q V Q L A A
W
10,26,43,68,83 CAG GTG CAG CTG --- --- --- --g g-- --a --- -c- --a --- --- --c --- --- --- --- --- --- --- --- --- --- --c --- --c --t --t -
--c tgg
(D)
N
14 (A) --- --- --a --a --- --- --- --g --- --- --- --- --- --- --- --- g-a --- --- --- -a- --- --t --t g-- --- --t -ac
aac
100 110 120 130 140 150 160 170 180 190
I I FR2 I
I CDR2 I
M H W V K Q K P G Q G L E W I G D I N P Y N D G T K Y N E K F
G>
49,50,69,90 ATG CAC TGG GTG AAG CAG AAG CCT GGG CAG GGC CTT GAG TGG ATT GGA GAT ATT AAT CCT TAC AAT GAT GGT ACT AAG TAC AAT GAG AAG TTC /
GGC
(B)
80 (C) ---
---
95 (I) ---

R Y S T G Y E Q
D
10,26,43,68,83 --- --- --- --a --a --- -g- --- --a --- --t --g --a --- --- --- t-c --- --- --- ag- -c- -g- ta- --- g-- --- --- c-- --- ---
--g -a-
(D) I H S H K S Y D S G S S Q
14 (A) --a t-- --- --- --- --- -gc -a- --a a-- a-t --- --- --- --- --- t-- --c g-- --- --- -g- -g- --- t-- -gc --- --c c-- --- --- --g
---

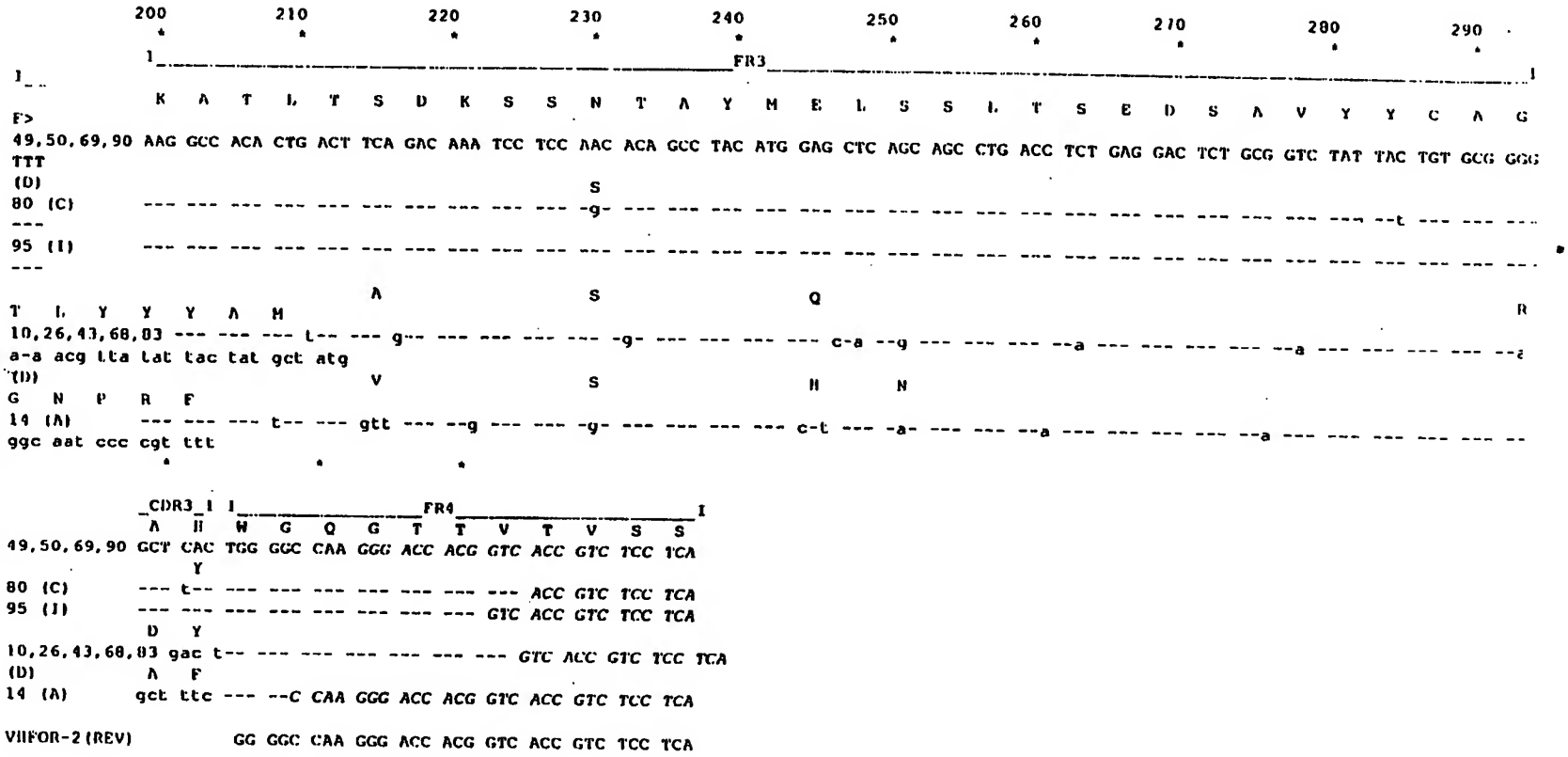


Figure 14

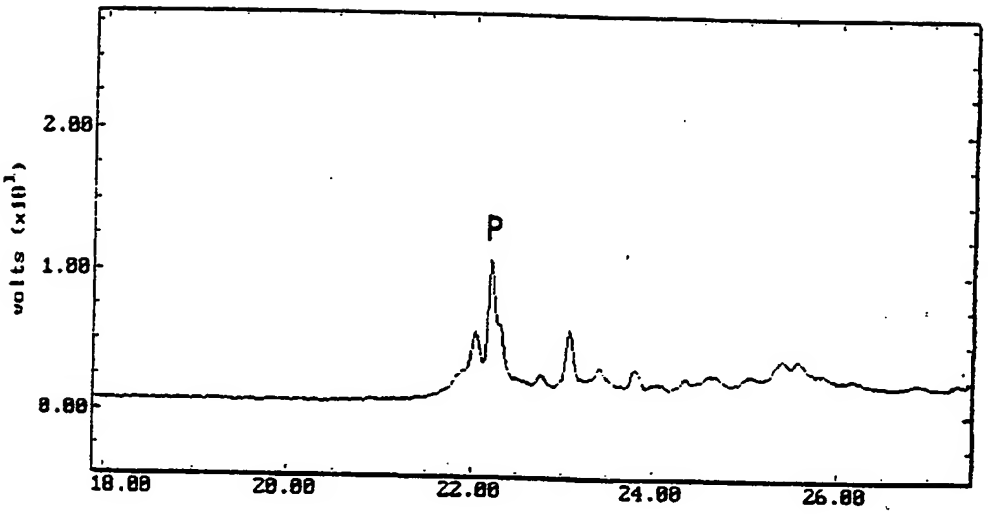


Figure 15A

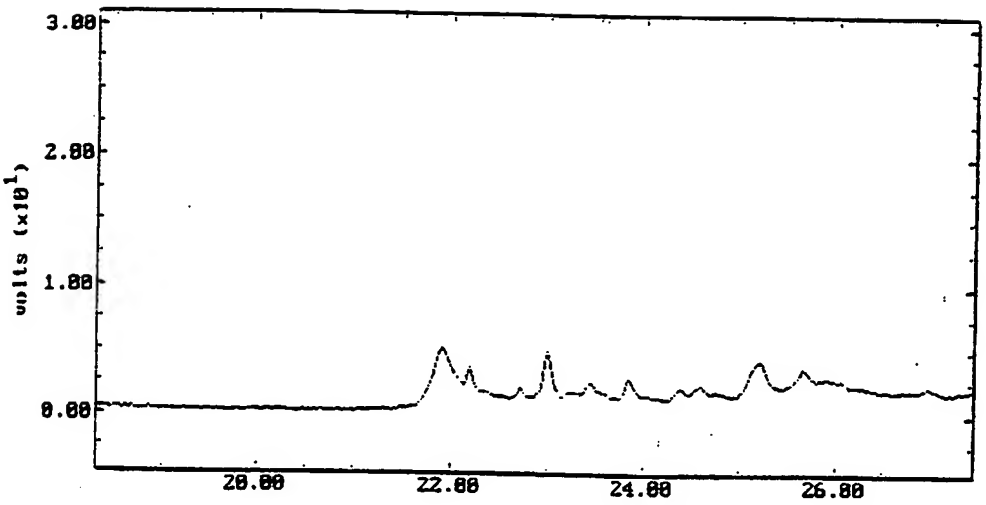


Figure 15B

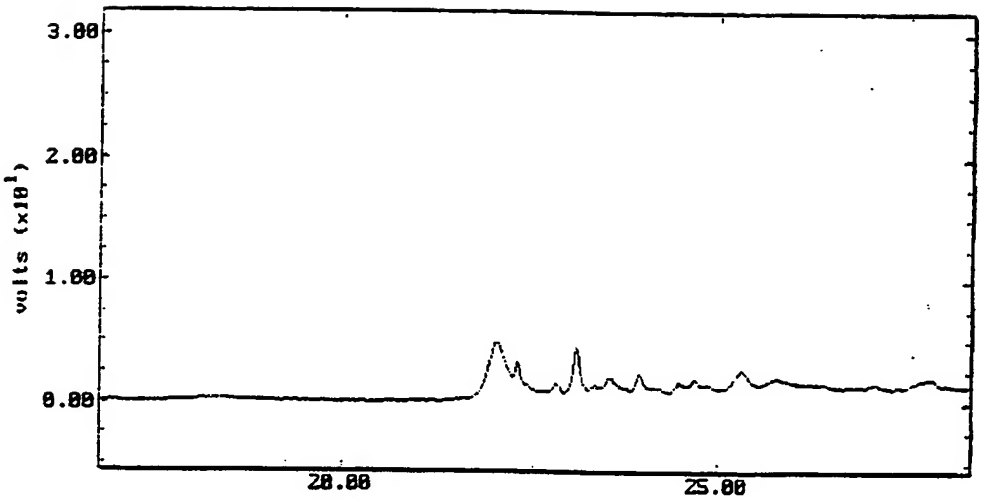


Figure 15C

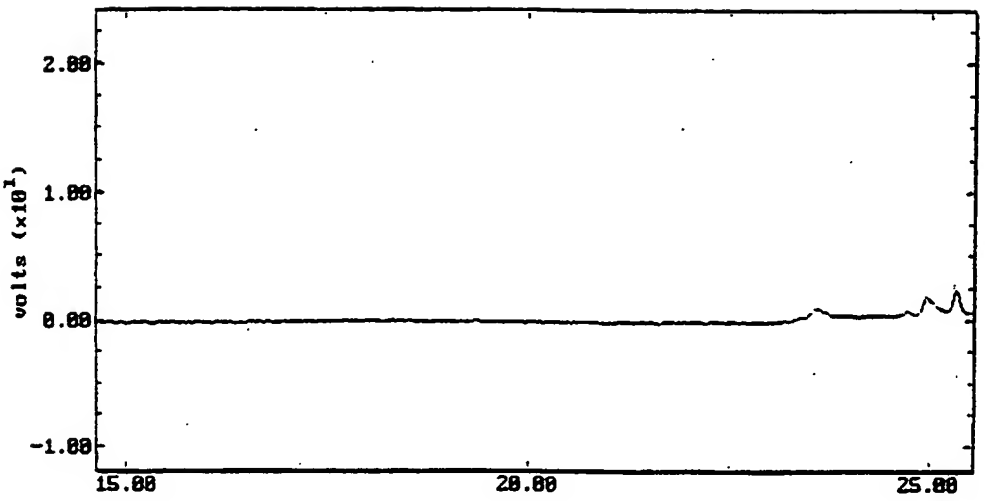


Figure 16

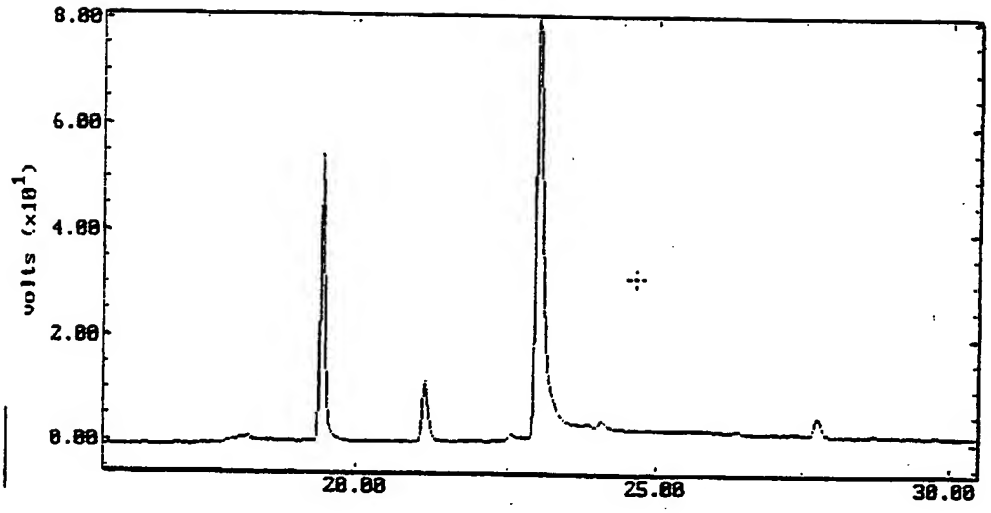


Figure 17A

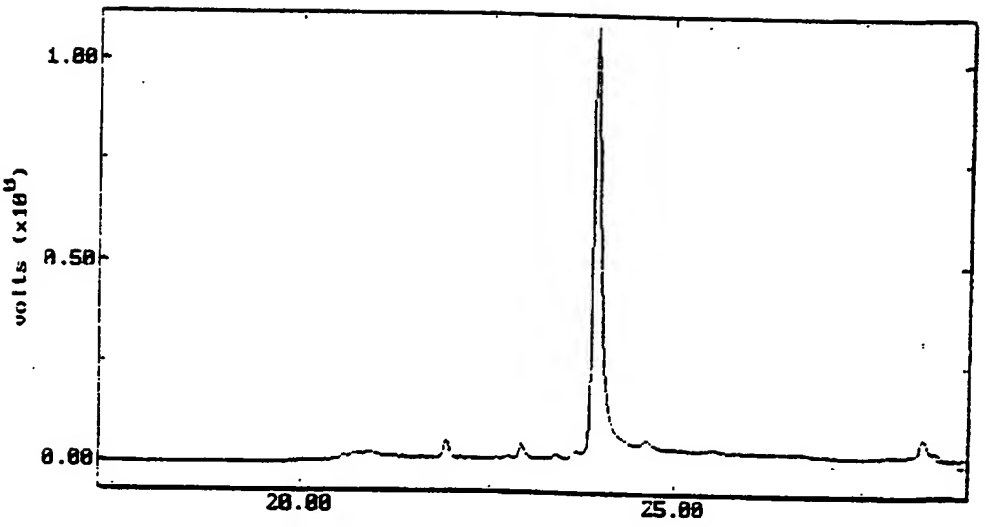


Figure 17B

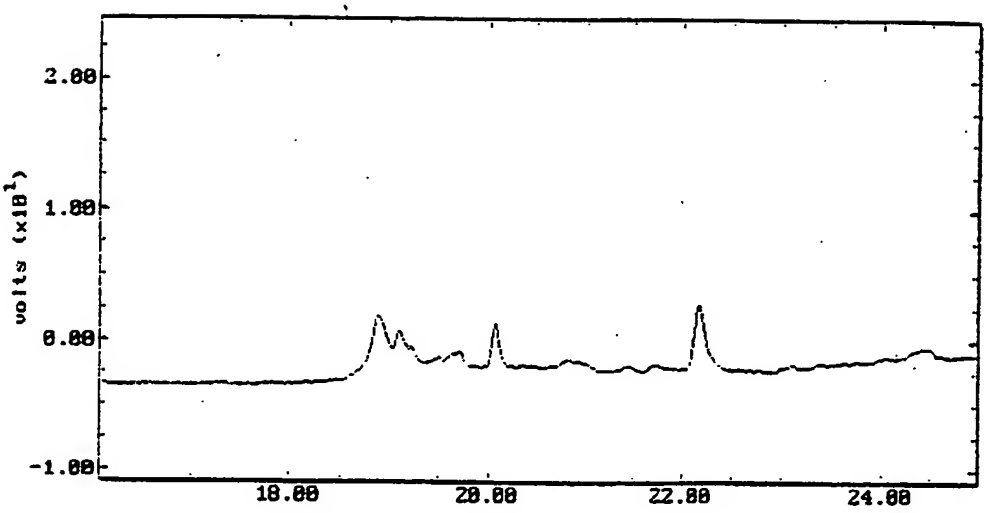


Figure 18

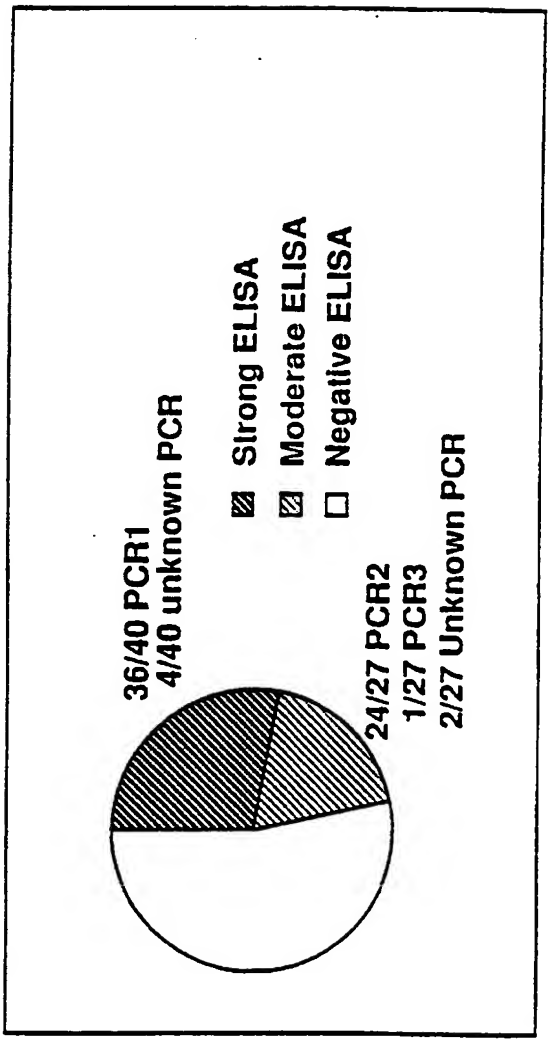

36/40 PCR1
4/40 unknown PCR
Strong ELISA
Moderate ELISA
Negative ELISA
24/27 PCR2
1/27 PCR3
2/27 Unknown PCR

Figure 19A

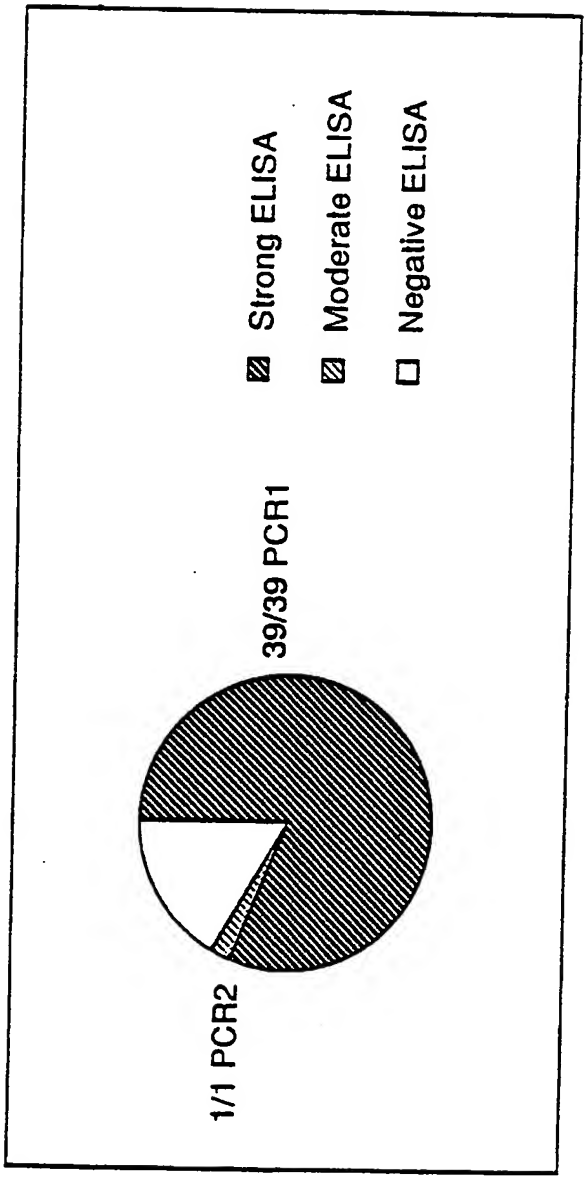

Strong ELISA
Moderate ELISA
Negative ELISA
39/39 PCR1
1/1 PCR2

Figure 19B

HEAVY CHAIN

FR 1 CDR 1 FR 2

GAA GTC TCC TGC AAG GCT TCT GGA GGC ACC TTC AGC AGC TAT GCT ATC AGC TGG
CTT CAG AGG ACG TTC CGA AGA CCT CCG TGG AAG TCG TCG ATA CGA TAG TCG ACC
Glu Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp

CDR 2

GTG CGA CAG GCC CCT GGA CAA GGG CTT GAG TGG ATG GGA GGG ATC AAC GCT GGC
CAC GCT GTC CGG GGA CCT GTT CCC GAA CTC ACC TAC CCT CCC TAG TTG CGA CCG
Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Asn Ala Gly

FR 3

AAT GGT AAC ACA AAA TAT TCA CAG AAG TTC CAG GGC AGA GTC ACC ATT ACC AGG
TTA CCA TTG TGT TTT ATA AGT GTC TTC AAG GTC CCG TCT CAG TGG TAA TGG TCC
Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Arg

GAC ACA TCC GCG AGC ACA GCC TAC ATG GAG CTG AGC AGC CTG AGA TCT GAA GAC
CTG TGT AGG CGC TCG TGT CGG ATG TAC CTC GAC TCG TCG GAC TCT AGA CTT CTG
Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp

ACA GCT GTG TAT TAC TGT
TGT CGA CAC ATA ATG ACA
Thr Ala Val Tyr Tyr Cys

LIGHT CHAIN

```
..................... FR 1                                          CDR 1
CAC CCT CAG CGT CTG GAC CCC GGG CAG AGG GTC ACC ATC TCT TGT TCT GGA AGC
GTG GGA GTC GCA GAC CTG GGG CCC GTC TCC CAG TGG TAG AGA ACA AGA CCT TCG
His Pro Gln Arg Leu Asp Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser

                                                  FR 2
AGC TCC AAC ATC GGA AGA AGT ACT GTA AGC TGG TAC CAG CAG CTC CCA GGC ACG
TCG AGG TTG TAG CCT TCT TCA TGA CAT TCG ACC ATG GTC GTC GAG GGT CCG TGC
Ser Ser Asn Ile Gly Arg Ser Thr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr

                    CDR 2                                  FR 3
GCC CCC AAA CTC GTC ATG TAT AGT CAC AAT CAG CGG TCC TCA GGG GTC CCT GAC
CGG GGG TTT GAG CAG TAC ATA TCA GTG TTA GTC GCC AGG AGT CCC CAG GGA CTG
Ala Pro Lys Leu Val Met Tyr Ser His Asn Gln Arg Ser Ser Gly Val Pro Asp

CGA TTC TCT GGC TCC AAG TCT GGC AAC TCA GCC TCC CTG GAC ATC AGT GGG CTC
GCT AAG AGA CCG AGG TTC AGA CCG TTG AGT CGG AGG GAC CTG TAG TCA CCC GAG
Arg Phe Ser Gly Ser Lys Ser Gly Asn Ser Ala Ser Leu Asp Ile Ser Gly Leu

                                  CDR 3
CAG TCT GAG GAT GAG GCT GAT TAT TAC TGT GCA GCA TGG GAT GAC AGC CTG AGT
CTC AGA CTC CTA CTC CGA CTA ATA ATG ACA CGT CGT ACC CTA CTG TCG GAC TCA
Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Ser

          FR 4
GAA TTT CTC TTC GGA ACT GGG ACC AAG GTC ACC GTC CTA GGT
CTT AAA GAG AAG CCT TGA CCC TGG TTC CAG TGG CAG GAT CCA
Glu Phe Leu Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly
```

HEAVY CHAIN

....FR 1 CDR 1

```
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTT AGC AGC TAT GCC ATG
AGG GAC TCT GAG AGG ACA CGT CGG AGA CCT AAG TGG AAA TCG TCG ATA CGG TAC
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
```

FR 2 CDR 2

```
AGC TGG GTC CGC CAG GCT CCA GGG AAG GGG CTG GAG TGG GTC TCA TCC ATT AGT
TCG ACC CAG GCG GTC CGA GGT CCC TTC CCC GAC CTC ACC CAG AGT AGG TAA TCA
Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
```

FR 3

```
AGT AGT AGT GGT GAC ACA TAC TAC GCA GAC TCA GTG AAG GGC CGA TTC ACC ATC
TCA TCA TCA CCA CTG TGT ATG ATG CGT CTG AGT CAC TTC CCG GCT AAG TGG TAG
Ser Ser Ser Gly Asp Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile

TCC AGA GAC AAC GCC CAG AAC TCA CTG TAT CTG CAA ATG AAC AGC CTG AGA GTC
AGG TCT CTG TTG CGG GTC TTG AGT GAC ATA GAC GTT TAC TTG TCG GAC TCT CAG
Ser Arg Asp Asn Ala Gln Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Val
```

CDR 3

```
GAG GAC ACG GCT GTT TAT TAC TGT GCG AGA GTC AGG GTT TAC AGC AGT GCC TGG
CTC CTG TGC CGA CAA ATA ATG ACA CGC TCT CAG TCC CAA ATG TCG TCA CGG ACC
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Val Arg Val Tyr Ser Ser Ala Trp
```

FR 4

```
GAC TAC TGG GGC CAG GGA ACC CTG GTC ACC GTC TCC
CTG ATG ACC CCG GTC CCT TGG GAC CAG TGG CAG AGG
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
```

LIGHT CHAIN

..FR 2 CDR 2 FR 3

```
GTA CTT GTC ATC TAT GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC CGA TTC
CAT GAA CAG TAG ATA CCA TTT TTG TTG GCC GGG AGT CCC TAG GGT CTG GCT AAG
Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe

TCT GGC TCC AGC TCA GGA AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG
AGA CCG AGG TCG AGT CCT TTG TGT CGA AGG AAC TGG TAG TGA CCC CGA GTC CGC
Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala
```

CDR 3

```
GAA GAT GAG GCT GAC TAT TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC CAT AGA
CTT CTA CTC CGA CTG ATA ATG ACA TTG AGG GCC CTG TCG TCA CCA TTG GTA TCT
Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Arg
```

FR 4

```
GTT GTT ACG GCC GGA GGG ACC AAG CTG ACC GTC CTA GGT
CAA CAA TGC CGG CCT CCC TGG TTC GAC TGG CAG GAT CCA
Val Val Thr Ala Gly Gly Thr Lys Leu Thr Val Leu Gly
```

HEAVY CHAIN

..FR 1

```
                                                                CDR 1
CTC GAG ACC CTG TCG CTC ACC TGC GCT GTC TCT GGT TAC TCC ACA CGG TTA CTA
GAG CTC TGG GAC AGC GAG TGG ACG CGA CAG AGA CCA ATG AGG TGT GCC AAT GAT
Leu Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Thr Arg Leu Leu
```

FR 2

```
                                                                CDR 2
CTG GCC TGG GTC CGG CAC CTC CCA GGG AAG GGG CTG GAG TGG ATT GGG AGT ATA
```

```
GAC CGG ACC CAG GCC GTG GAG GGT CCC TTC CCC GAC CTC ACC TAA CCC TCA TAT
Leu Ala Trp Val Arg His Leu Pro Gly Lys Gly Leu Glu Trp Ile Gly Ser Ile

                                                                  FR 3
CAT CAT AGT GGG CCC ACC TAC TAC AAC CCG TCC CTC AAG AGT CGA GTC ACC ATG
GTA GTA TCA CCC GGG TGG ATG ATG TTG GGC AGG GAG TTC TCA GCT CAG TGG TAC
His His Ser Gly Pro Thr Tyr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met

TCA CCT GAC ACG TCC AGG AAC CAG TTC TCC CTG AAG ATG ACC TCT GTG ACC GCC
AGT GGA CTG TGC AGG TCC TTG GTC AAG AGG GAC TTC TAC TGG AGA CAC TGG CGG
Ser Pro Asp Thr Ser Arg Asn Gln Phe Ser Leu Lys Met Thr Ser Val Thr Ala

                                                  CDR 3
GCG GAC ACG GCC ATG TAT TAC TGT GCG AGG GAC CGA TAT GGT TAC TTT GAC TCC
CGC CTG TGC CGG TAC ATA ATG ACA CGC TCC CTG GCT ATA CCA ATG AAA CTG AGG
Ala Asp Thr Ala Met Tyr Tyr Cys Ala Arg Asp Arg Tyr Gly Tyr Phe Asp Ser

FR 4
TGG GGC CAG GGA ACC CTG GCC ACC GTC TC
ACC CCG GTC CCT TGG GAC CGG TGG CAG AG
Trp Gly Gln Gly Thr Leu Ala Thr Val Ser
```

LIGHT CHAIN

```
FR 1                                                              CDR 1
CCT GCT TGG TTG CTT GTG GCC TTG GGA CAG ACA GTC AGG ATC ACA TGC CAA GGA
GGA CGA ACC AAC GAA CAC CGG AAC CCT GTC TGT CAG TCC TAG TGT ACG GTT CCT
Pro Ala Trp Leu Leu Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly

                                                  FR 2
GAC AGC CTC AGA AGT TAT TAT GCA AGT TGG TAT CAG CAG AAG CCA GGA CAG GCC
CTG TCG GAG TCT TCA ATA ATA CGT TCA ACC ATA GTC GTC TTC GGT CCT GTC CGG
Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala
```

CDR 2 FR 3

```
CCT GTA CTT GTC ATC TCT GGT AAA AAC AAC  CGG CCC TCA GGG ATC CCA GAC CGA
GGA CAT GAA CAG TAG AGA CCA TTT TTG TTG  GCC GGG AGT CCC TAG GGT CTG GCT
Pro Val Leu Val Ile Ser Gly Lys Asn Asn  Arg Pro Ser Gly Ile Pro Asp Arg

TTC TCT GCC TCC AGC TCA GGA AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CAG
AAG AGA CGG AGG TCG AGT CCT TTG TGT CGA AGG AAC TGG TAG TGA CCC CGA GTC
Phe Ser Ala Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln
```

CDR 3

```
GCG GAA GAT GAG GCT GAC TAT TAC TGT CTC TCT CGG GAC AGC GGA AGT AAC CAA
CGC CTT CTA CTC CGA CTG ATA ATG ACA GAG AGA GCC CTG TCG CCT TCA TTG GTT
Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Leu Ser Arg Asp Ser Gly Ser Asn Gln
```

FR 4

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CTG GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT
GAC CAT AAG CCG CCT CCC TGG TTC GAC TGG CAG GAT CCA
Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
```

Figure 20

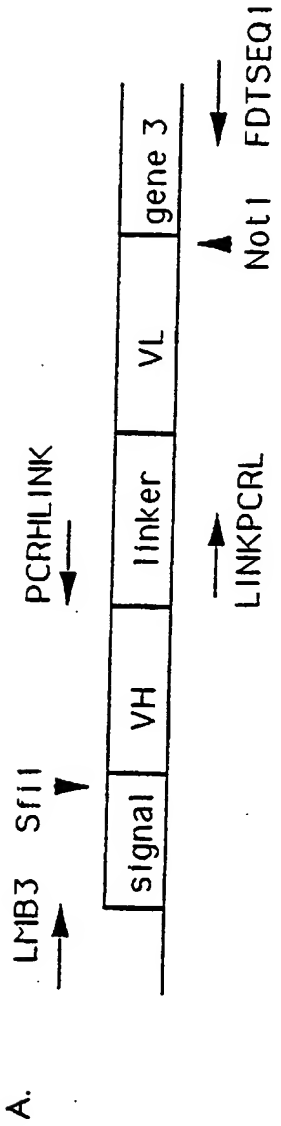
A.
LMB3
SfiI
signal
VH
linker
PCRHLINK
LINKPCRL
VL
NotI
gene 3
FDTSEQ1

Figure 21

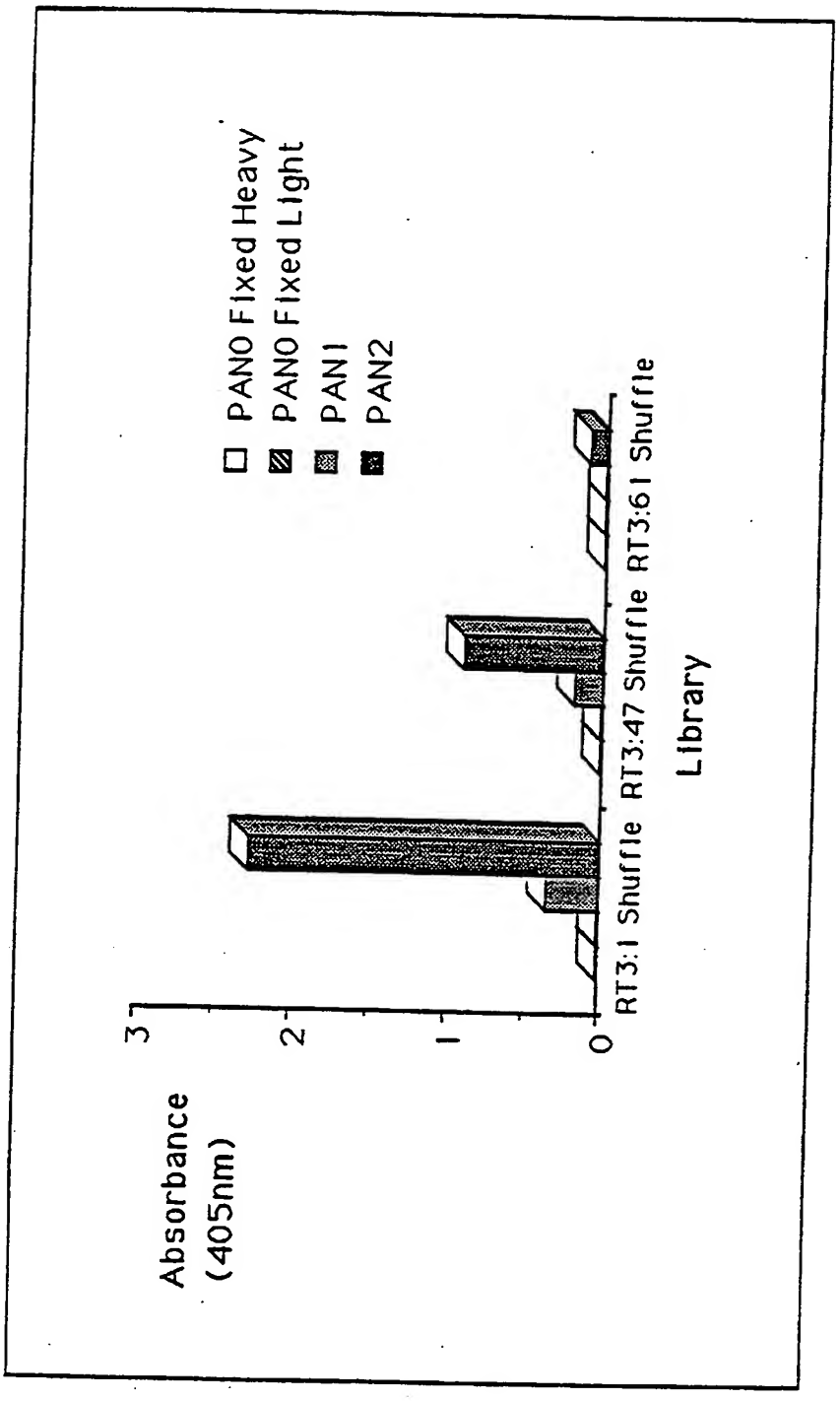
PANO Fixed Heavy
PANO Fixed Light
PAN1
PAN2
Absorbance (405nm)
3
2
1
0
RT3:1 Shuffle
RT3:47 Shuffle
RT3:61 Shuffle
Library

Figure 22

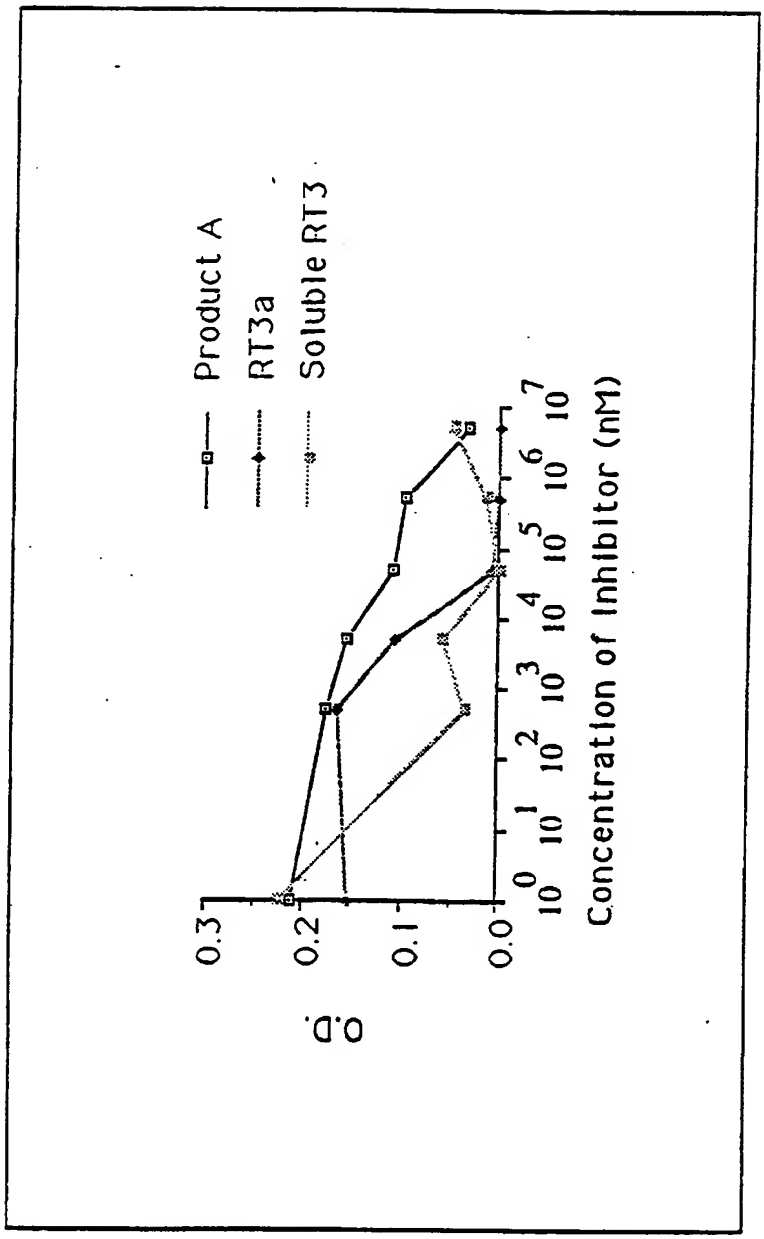
Product A
RT3a
Soluble RT3
O.D.
0.3
0.2
0.1
0.0
10^0 10^1 10^2 10^3 10^4 10^5 10^6 10^7
Concentration of Inhibitor (nM)

Figure 23A

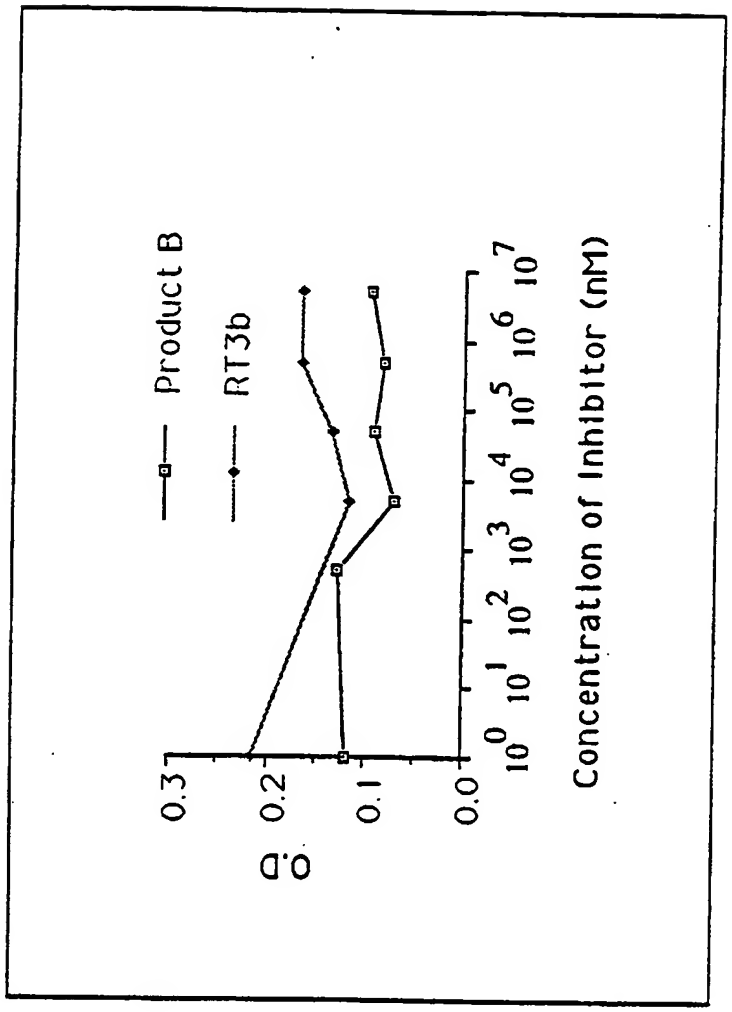
Product B
RT3b
O.D
0.3
0.2
0.1
0.0
10^0 10^1 10^2 10^3 10^4 10^5 10^6 10^7
Concentration of Inhibitor (nM)

Figure 23B

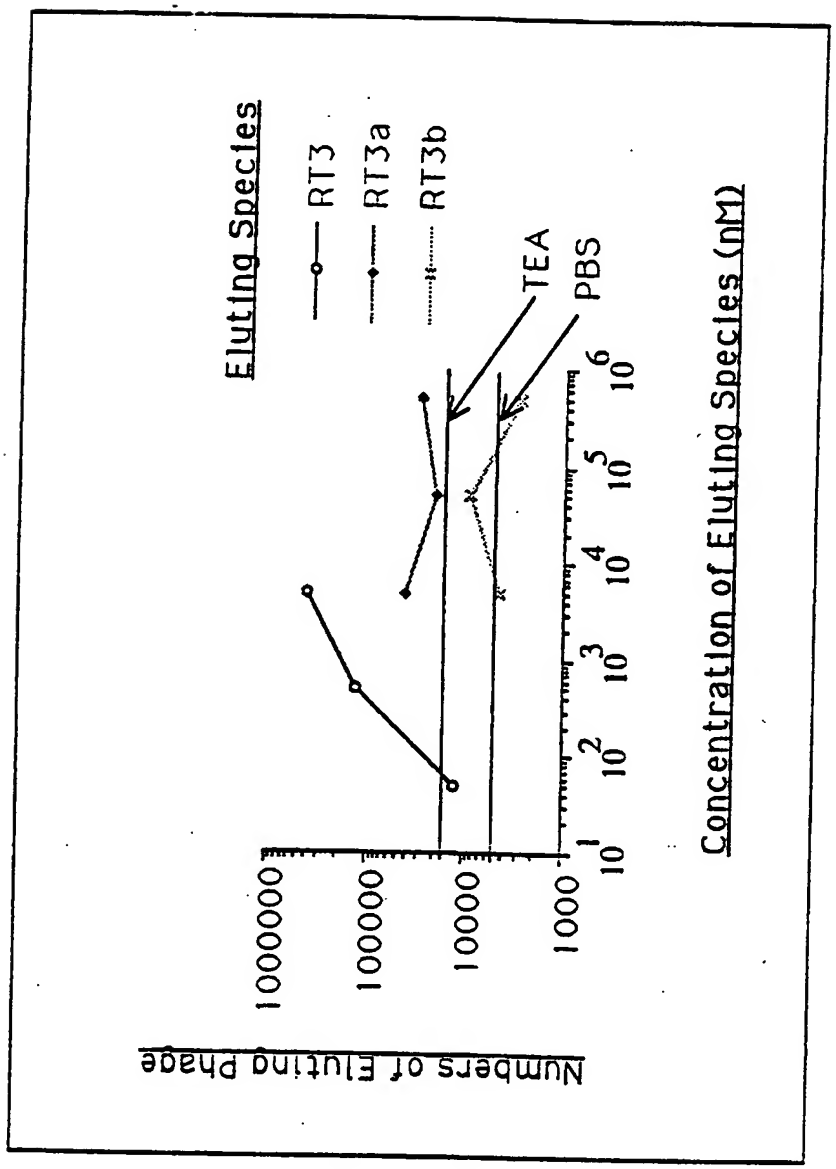
Eluting Species
RT3
RT3a
RT3b
TEA
PBS
Concentration of Eluting Species (nM)
Numbers of Eluting Phage
1000000
100000
10000
1000
10^1
10^2
10^3
10^4
10^5
10^6

Figure 24A

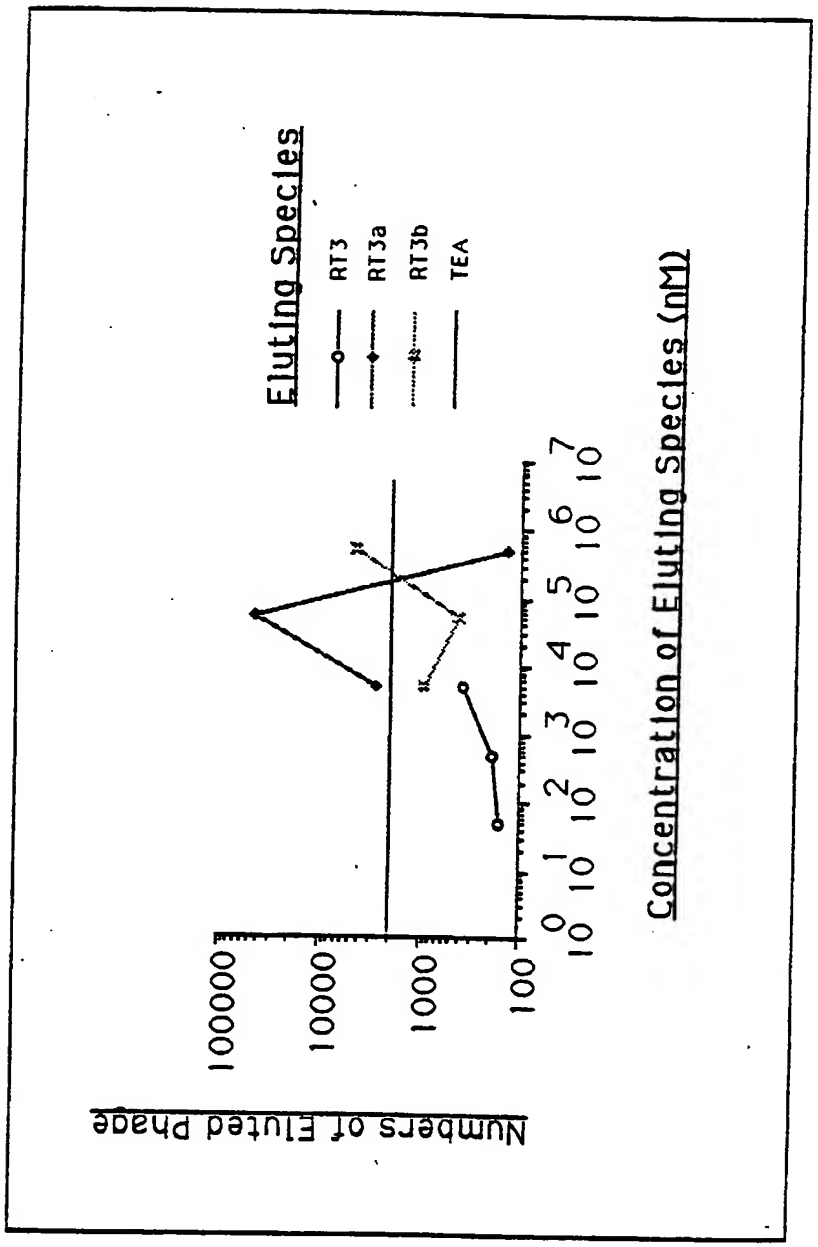
Eluting Species
RT3
RT3a
RT3b
TEA
Numbers of Eluted Phage
100000
10000
1000
100
Concentration of Eluting Species (nM)
0 1 2 3 4 5 6 7
10 10 10 10 10 10 10 10

Figure 24B

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US94/03420

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) :C12N 9/00; A61K 37/48
US CL :435/188.5; 424/135.1
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/188.5; 424/135.1; 530/387.3, 389.8

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	SCIENCE, VOLUME 245, ISSUED 08 SEPTEMBER 1989, E. BALDWIN, ET AL., "GENERATION OF A CATALYTIC ANTIBODY BY SITE-DIRECTED MUTAGENESIS", PAGES 1104-1107, SEE ENTIRE DOCUMENT.	1-20, 24-29
Y	SCIENCE, VOLUME 246, ISSUED 08 DECEMBER 1989, W. D. HUSE, ET AL., "GENERATION OF A LARGE COMBINATORIAL LIBRARY OF THE IMMUNOGLOBULIN REPERTOIRE IN PHAGE LAMBDA", PAGES 1275-1281, SEE ENTIRE DOCUMENT.	1-20, 24-29
Y	BIO/TECHNOLOGY, VOLUME 10, ISSUED JULY 1992, J. D. MARKS, ET AL., "BY-PASSING IMMUNIZATION: BUILDING HIGH AFFINITY HUMAN ANTIBODIES BY CHAIN SHUFFLING", PAGES 779-783, SEE ENTIRE DOCUMENT.	1-20, 24-29

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search	Date of mailing of the international search report
09 SEPTEMBER 1994	16 SEP 1994
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer Charles Patterson Jill Warden for Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US94/03420

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	NUCLEIC ACIDS RESEARCH, VOLUME 19, NO. 15, ISSUED 1991, H. R. HOOGENBOOM, ET AL., "MULTI-SUBUNIT PROTEINS ON THE SURFACE OF FILAMENTOUS PHAGE: METHODOLOGIES FOR DISPLAYING ANTIBODY (FAB) HEAVY AND LIGHT CHAINS, PAGES 4133-4137, SEE ENTIRE DOCUMENT.	1-20, 24-29
Y	NATURE, VOLUME 352. ISSUED 15 AUGUST 1991, T. CLACKSON, ET AL., "MAKING ANTIBODY FRAGMENTS USING PHAGE DISPLAY LIBRARIES", PAGES 624-628, SEE ENTIRE DOCUMENT.	1-20, 24-29
Y	J. MOL. BIOL., VOLUME 222, ISSUED 1991, J. D. MARKS, ET AL., "BY-PASSING IMMUNIZATION, HUMAN ANTIBODIES FROM V-GENE LIBRARIES DISPLAYED ON PHAGE", PAGES 581-597, SEE ENTIRE DOCUMENT.	1-20, 24-29
Y	NATURE, VOLUME 348, NO. 6301, ISSUED 06 DECEMBER 1990, J. MCCAFFERTY, ET AL., "PHAGE ANTIBODIES: FILAMENTOUS PHAGE DISPLAYING ANTIBODY VARIABLE DOMAINS", PAGES 552-554, SEE ENTIRE DOCUMENT.	1-20, 24-29